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Pebruary 4, 2005, 11:54:40 ; Search time 147.676 Seconds
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2005
                                                                    sw model
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Gapop 10.0 , Gapext 0.5
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1696
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* Database

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

geneseqp2001s:*
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geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	SCZ/CD84.	an CD8	an PRO	an leu	an sof	PRO polyp	an sec	an nov	Region of	el hum	an sec	an 5'	an imm	an imm					an Ly-	an Ly-	Dendritic	an CD2	Hypoxia-i	an CD2	an CD2
Ę.	SCZ,	Human	Human	Human	Human	PRO	Human	Human	Reg	Novel	Human	Den	Human	H	Human	Human									
Description	Aab47878	Aae26238	Ad182907	Ado05708	Adq19067	Adp23943	Aaw74891	Abg95343	Abo34537	Adi23198	Adh74200	Aay12524	Abg96270	Adk98560	Aau74425	Ad157243	Ad157105	Ad157103	Ado63782	Ado78174	Aae12078	Aae26243	Abp65110	Abw01823	Aae26250
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gi Gi	AAB47878	AAE26238	ADL82907	AD005708	ADQ19067	ADP23943	AAW74891	ABG95343	AB034537	ADI23198	ADH74200	AAY12524	ABG96270	ADK98560	AAU74425	ADL57243	ADL57105	ADL57103	AD063782	AD078174	AAE12078	AAE26243	ABP65110	ABW01823	AAE26250
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Score	1695	1695	1695	1695	1695	1695	1695	1695	1695	1695	1695	411	382.5	382.5	382.5	378.5	378.5	378.5	374	374	373	373	373	373	370
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Aae26251 Human CD2 Aae26252 Human CD2 Abw01830 Human CD2 Abw01831 Human CD2	Abw01832 Human CD2 Aae26253 Human CD2 Abw01833 Human CD2 Aau09868 Novel hum	Membra Human Human	Human APEX-1 Human	Abussass human Pec Abussass Human PRO Abussass Novel hum Abussass Human sec Abre6232 Human sec
AAE26251 AAE26252 ABW01830 ABW01831	ABW01832 AAE26253 ABW01833	AAY66701 AAY70431 AAY44609	AA029119 AAB87548 AAB87321 AAB65224	ABC95873 ABU58495 ABU88043 ABU84358 ABR66232
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ALIGNMENTS

Diagnosing susceptibility to schizophrenia (SC2) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1q22, were the marker is linked to a variant SCZ; CD84; platelet; monocyte; circulating B cell; schizophrenia; allele; polymorphic marker; chromosome 1q22. (RUTF) UNIV RUTGERS STATE NEW JERSEY. Ą AAB47878 standard; protein; 328 23-APR-2001; 2001WO-US013040. 21-APR-2000; 2000US-0198873P. Brzustowicz LM, Bassett AS; (first entry) form of the SCZ gene. WPI; 2002-171605/22. N-PSDB; AAI72383. WO200202054-A2. Homo sapiens 10-JAN-2002. 02-MAY-2002 AAB47878; SCZ/CD84. RESULT 1 AAB47878

Example 6; Page 70; 82pp; English.

This sequence is encoded by the SCZ gene which was isolated using the method of the invention. The SCZ gene has been previously identified as CD84, GenBank Accession No: NM 003874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. This protein may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method of diagnosing susceptibility to schizophrenia in a patient. The method comprises determining the presence or absence of an allele of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1q22 and is linked to a gene (SCZ) having

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                                                                                                                                                                                       AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                                                                         1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                MAQHHLMILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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                                                                                               Gaps
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0
                                                                Length 328;
   a variant form associated with a phenotype of schizophrenia
                                                                                            Indels
                                                            99.9%; Score 1695; DB 5;
100.0%; Pred. No. 8e-138;
ive 0; Mismatches 0;
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                                                                            llarity 100.0%; Pr
Conservative 0;
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N-PSDB; AAD43563.
                                                        Query Match
Best Local Similarity
Matches 328; Conserv
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                              Sequence 328 AA;
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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains and SIAMA associated protein (SAP) motifies. CD2000 DNA and protein is cuseful for treating disorder such as immune proliferative disorders, useful for treating disorder such as immune proliferative disorders (e.g. carcinomal, viral infection, autoimmune disorders (e.g. archivitis, multiple sclerosis, Grave's disease, and Hashimoto's (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashimoto's clissase). T cell disorder (e.g. acquired immune deficiency syndrome (C. MIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), inflammatory disorders (e.g. rheumatory disorders, septic shock, costeoarthritis), allergic inflammatory disorders (e.g. asthma and psoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cyctoxic disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cirrhosis, cachexia, jaundice, hepatic circulacory disorders, hepaticis, cirrhosis, cachexia, jaundice, hepatic circulacory disorders, hepaticis, cirrhosis, cachexia, jaundice, hepatic circulacory disorders, cachexia, jaundice, hepatic circulacory disorders, pepaticis, cirrhosis, cachexia, jaundice, hepatic circulacory disorders, pepaticis, circhosis, cachexia, jaundice, hepatic suseful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive crials and phramacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 protein
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Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
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                                                                                           Disclosure; Page 76-77; 138pp; English
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The invention relates to treating a subject having a condition that benefits from modulating the balance of regulatory T cell function.

CC benefits from modulating the balance of regulatory T cell function to relative to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1, CG PR-32, CD84, CD89, SECTONIA, RZC, GRR63, PG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-3, PSG-6, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-1, PSG-1, PSG-9, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-1, PSG-1, PSG-9, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-1, PSG-1, PSG-9, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-1, PSG-9, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-9, PSG-9, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-1, PSG-9, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-9, PSG-9, PSG-9, PDE-4d, and PI-1, PSG-1, PSG-9, PSG-9, PSG-9, PDE-4d, and PSG-9, PSG
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                                                                                                                                                                                                                                 T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; CD83; leukocyte differentiation antigen.
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                                                                                                                                                                                    Human leukocyte differentiation antigen CD84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; SEQ ID NO 8; 161pp; English.
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                         ADO05708 standard; protein; 328
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09-OCT-2002; 2002US-0417103P.
09-OCT-2002; 2002US-0417243P.
18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424777P.
08-NOV-2002; 2002US-0424881P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-2003; 2003WO-US032065
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Best Local Similarity 100.
Matches 328; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jagged-1 or GPR-32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Szymanska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADO05707.
GENBANK; 6650105.
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                                                                                                                                                                                                                                                                                                                                                                                                             WO2004032867-A2.
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-2004.
                                                                             ADO05708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rao P,
AD005708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, eg. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency selective IgA deficiency immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's Iyamphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or anytiosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and come mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondyllitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKRYNLOIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEBKNVTYNWSPLGEEGNVLQI
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                                                                                                                                                                                                                                                                                                                                Wood WI;
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                                                                                                                                                                                                                                                                                                                                Schoenfeld JR,
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                                                                                                                                                                                                                                                                                                                                Fong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Fig 109; 695pp; English
                                                                                                                                                                                                                                                                                                                                   Dennis K,
                                                                                                                                                                   15-SEP-2003; 2003WO-US029097
                                                                                                                                                                                                                      16-SEP-2002; 2002US-0411392P
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Matches 328; Conservative
                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-329389/30.
                                                                                                                                                                                                                                                                                                                                   Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADL82906
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                                                      WO2004024097-A2.
     Homo sapiens.
                                                                                                            25-MAR-2004
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Length 328; 0; Indels

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the of protein expression in the first soft tissue sample indicates the cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic saric sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
               TKRYNLOIYERLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLOI 180
                                                                                   SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
                                                                                                                                                      soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                 FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVBKBEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                                                                                         - SEQ ID 1886.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human soft tissue sarcoma-upregulated protein
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                                                                                                                                                                                                                          EVQFADKMGKASTQDSKPPGTSSYEIVI 328
                                                                                                                                                                                                                                                                                                                           ADQ19067 standard; protein; 328 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROT-) PROTEIN DESIGN LABS INC
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                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antithemutalc, immunosuppressive, osteopathic, antidabetic, dermatological, antipsoriatic, antiallergic, antiatematic, hepatocropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                          241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS
                           1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                             TKRYNLOIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                              PQTPEDQELTYTCTAQNPVSNNSDS1SARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
                                                                                                                                                                                                                                                                                                                                                                            181 FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFPLLVLIL
MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 7; SEQ ID NO 1121; 2940pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQFADKMGKASTQDSKPPGTSSYEIVI
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Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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N-PSDB; ADP23942.
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ADP23943
ADP23943
ACC ADP23
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    idiopathic inflammatory myopathy, Sjogren's syndrome, systemic clatopathic inflammatory myopathy, Sjogren's syndrome, systemic clatopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous carbonic inflammatory demyelinating polymeuropathy, dullain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary cirlhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, a autoimmune or immune-mediated skin disease, autoimmune or immune-mediated skin disease, asthma, allargic rhintis, atopic dermatitis, food whypersensitivity, urticaria, an immunologic disease, of the lung, consumential subministic desirential indication associated disease, graft rejection or context desirents a proper sensitivity of the context desirents a proper sensitivity of the context desirents a proper sensitivity of the context desirents and the context desirents a proper sensitivity of the context desirents and the context desi
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fusion protein; cancer; central nervous system; seizure; diagnosis;
neurodegenerative disease.
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                                                            TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTVNWSPLGEEGNVLQI
                                                                            TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
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                        AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
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      AYVTPGDSETAPVVTVTHRNYYER I HALGPNYNLVI SDLRMEDAGDYKAD I NTQADPYTT
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N-PSDB; AAV59674.
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22-AUG-1997;
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, by bacteria, viruses and fungi and ocular disorders infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound cauburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The collure of primary tissues, to regenerate tissues and in chemotaxis. C.c. increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents one of the novel human created proteins of the invention. Note: This sequence did not form of the printed specification, but was obtained in electronic format correctly from USPTO at seqdata.usptc.gov/sequence.html?
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                                                                                                                     , Rosen CA, Fischer CL, Soppet DP, Carter KC;
DK, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
M, Duan Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                      New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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100.0%; Pred. No. 8.1e-138;
iive 0; Mismatches 0;
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97US-0058785P.
                  97US-0061060P.
98WO-US004493.
                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 328; Conservative
                                                                                                                                                                                                                        WPI; 2002-634796/68.
                                                                                                                                                           Ferrie AM, Duan R
Moore PA, Shi Y,
                                                                                                                                                                                                                                             N-PSDB; ABS73661.
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  12-SEP-1997;
02-OCT-1997;
06-MAR-1998;
                                                                                                                     Ruben SM,
Bednarik D
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9703-0047614P.
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9703-0056874P.
9703-0056878P.
9703-0056888P.
97US-0047593P
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
YU G.
NI J.
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23-MAY-1997;
23-MAY-1997;
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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(ENDR/)
(YUGG/)
(NIJJ/)
Human; secreted protein; hyperproliferative disorder; leukaemia;

breast cancer; wound; reproductive disorder; blood-related disorder;

haemophilia; thrombocytopaemia; immunodeficiency; thymic hypoplasia;

Wiskott-Aldrich syndrome; auttoimmune disorder; multiple sclerosis;

W viral infection; bacterial infection; fungal infection; AIDS; sepsis;

renal disorder; kidney failure; cardiovascular disorder; cytostatic;

W angina pectoris; cerebral isohaemia; congenital heart defect;

respiratory disorder; neurological disorder; Alzheimer's disease;

W Parkinson's disease; inflammation; Crohn's disease; vulnerary;

immunosuppressive; antibacterial; haemostatic; thrombolytic;

anticoagulant; neuroprotective; thyromimetic; antiallergic;

antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;

cerebroprotective; cardiant; nootropic; antiparkinsonian;

antiinflammatory.
                                                                              Region of human secreted protein encoded by cDNA sequence #164.
                        ABO34537 standard; protein; 329 AA
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97US-0040163P.
97US-0040331P.
97US-0040334P.
97US-00403311P.
97US-0043311P.
97US-0043311P.
97US-0043313P.
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97US-0043563P.
97US-0043674P.
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97US-0043674P.
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97US-0047589P.
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97US-0047588P.
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97US-0047588P.
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                                                            (first entry)
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                                                                                                                                                                                                                                               Homo sapiens.
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07-MAR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
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11-APR-1997;
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                                          ABO34537;
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     RESULT 9
               ABO3453
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FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
                181 PQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
                                                     SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS
                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; cancer; human; secreted protein.
                                                                                                                         EVQFADKMGKASTQDSKPPGTSSYELVI 328
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                                                                                                                                                                                                    ADI23198 standard; protein; 329 AA
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970S-0047502P.
970S-0047503P.
970S-0047581P.
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97US-0040163P.
97US-0040333P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention relates to the isolation of novel human secreted
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                                                                                                                                                                                                                                             Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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Pred. No. 8.1e-138;
0; Mismatches 0; Indels (
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100.0%; Pre
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Matches 328; Conservative
                                                                                   FLORENCE K A.
                                                                                                                        EBNER R.
BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
                                                                                                   OLSEN H S.
FISCHER C L.
      FENG P.
YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
                                                                                                                                                                                                                                                                                                                   WPI; 2003-521800/49.
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KYAW H.
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      (FENG/)
(YOUN/)
(GREE/)
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(KYAW/)
                                                                                   (FLOR/)
(OLSE/)
(FISC/)
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(YOUN/) (GREE/)

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970S-00476113P
970S-00476113P
970S-00476113P
970S-00476113P
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970S-005681P
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
                                   23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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22-AUG-1997;
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06-JUN-1997;
06-JUN-1997;
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22-AUG-1997
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(SOPP/)
(CART/)
(BEDN/)
(ENDR/)
(YUGG/)
(NIJJ/)
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The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a polypucleotide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a) -(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The is the amino acid sequence of a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                JM, Ferrie AM;
Ebner R;
1g Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEFRQVKIIAWTSKTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.9%; Score 1695; DB 7; Length 329; Best Local Similarity 100.0%; Pred. No. 8.1e-138; Matches 328; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP, Bodfress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Duan DR, Hu J, Plorence KA, Olsen HS, Fischer CL, Ebber Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z,
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YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
HU J.
HU J.
FICORENCE K A.
OLSEN H S.
FICORENCE C L.
BREWER L A.
BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
ZENG Z.
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N-PSDB; ADI22889.
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120 180 180 240 240

300

YU G. NI J. FENG P.

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human; secreted protein; cancer; haematopoietic disorder; endocrine disorder; immune system disease; inflammatory disorder.
                 ADH74200 standard; protein; 329 AA
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970S-0040161P

970S-0040163P

970S-0040333P

970S-0040334P

970S-0040331P

970S-0043311P

970S-0043312P

970S-0043313P

970S-0043313P

970S-0043318P

970S-0043568P

970S-0043508P

970S-0043508P
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97US-0047614P.
97US-0047615P.
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                                                                    Human secreted protein #164.
                                                   25-MAR-2004 (first entry)
                                                                                                                                   US2003225248-A1.
                                                                                                                  Homo sapiens.
                                                                                                                                                                      10-JUN-2002;
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11-APR-1997;
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RESULT 11
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Carter KC, Bednarik DP; Greene JM, Ferrie AM;
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Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AV
Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
     9705-0047618P

9705-0047618P

9705-0048944P

9705-0048974P

9705-0051926P

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9705-005631P

9705-0056631P

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Ni J,
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N-PSDB; ADH73891.
                                                     08-JUL-1997;
16-JUL-1997;
18-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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23-MAY-1997;
06-JUN-1997;
06-JUN-1997;
13-JUN-1997;
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06-MAR-1998
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The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPs) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoistic disorders, endocrine disorders, diseases of the immune system, inflammatory disorders and many others. Full details of disorders that may be

Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with aberrant expression and activity.

Claim 11; SEQ ID NO 483; 142pp; English.

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prevented, diagnosed and/or treated by the above methods are given in the proteins. The nucleic acid molecules may be used to produce their proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The SPs may also be used as antigens in the production of antibodies against the proteins and assays to identify modulators of SP expression and activity. The anti-SP antibodies may also be used to down regulate expression and activity. The neti-SP antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The present sequence represents the amino acid sequence of a human secreted protein.
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Sequence 329 AA;

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                                                                                                                                       61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
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                                     Gaps
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99.9%; Score 1695; DB 8; Length 329; 100.0%; Pred. No. 8.1e-138; ive 0; Mismatches 0; Indels
                              Indels
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                Best Local Similarity 100.
Matches 328; Conservative
 Query Match
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Human 5' EST secreted protein SEQ ID NO: 189 from WO 9906553. AAY12524 standard; protein; 79 AA (first entry) 22-JUN-1999 AAY12524;

Human, secreted protein, EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; antiinflammatory; tumour inhibition; antitumour.

Homo sapiens

WO9906553-A2

98WO-IB001237. 31-JUL-1998;

97US-00905051 01-AUG-1997;

(GEST) GENSET

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human secreted proteins, and encode the proteins given in AAY1250 to human secreted proteins, and encode the proteins given in AAY1251 to AAY12669, respectively. The proteins given represent the signal peptide and an N-terminal fragmen of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for disquesis and therapy. The proteins obtained may have cytokine activity, call proteins obtained may have cytokine activity, call proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, antiinflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acides encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
                                                                                                                                         New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from umbilical cord, lymph ganglia, lymphocytes and
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                      Lacroix B;
                      Duclert A,
                                                                                                                                                                                                                                        Claim 34; Page 323; 411pp; English.
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                      Dumas Milne Edwards J,
                                                                   WPI; 1999-153783/13.
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nes 78; Conserv
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Immunoglobulin superfamily protein; IGSFP; cell proliferative disorder; arteriosclerosis; atherosclerosis, cirrhosis; hepatitis; paroxystamal nocturnal hemoglobinuria; polycythaemia vera; psoriasis; primary thrombocytopenia; cancer; leukaemia; lymphoma; sarcoma; myeloma; autoimmune disorder; inflammatory disorder; lowphoma; sarcoma; myeloma; autoimmune thyroiditis; contact dermatitis; Crohn's disease; disbeficiency syndrome; AIDS; allergy; anaemia; asthma; autoimmune thyroiditis; contact dermatitis; Crohn's disease; disbeficiency strongerial; goodpasture syndrome; gout; draves' disease; Hashimoto's thyroiditis; irritable bowel syndrome; multiple sclerosis; osteoarthritis; osteoprosis; pancreatitis; multiple sclerosis; extendarial infection; fungal infection; uveitis; trauma; viral infection; brotozoal infection; helminthic infection; Human immunoglobulin superfamily protein IGSFP-8.

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ABG96270 standard; protein; 551

RESULT 13 ABG96270

11-DEC-2002 (first entry)

ABG96270;

Homo sapiens

gene

WO200272794-A2

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YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated immune response associated protein (IRAP) comprising any of 35 fully defined sequences given in the specification. The polypeptide of the invention demonstrates antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, cerebroprotective, antiinflammatory, nootropic and vasotropic activities and may be useful for treating a disease or condition associated with decreased expression or overexpression of functional immune response associated proteins, while the antibody is useful for diagnosing a condition or disease associated with the aspression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease and Crohn's disease. Furthermore, the molecules of the invention may be utilised during gene therapy incredures. The current sequence is that of a human IRAP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated immune response associated proteins (IRAP) polypeptide and polynucleotide, useful for diagnosing and/or treating disorders with aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA
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                                                                                                                                                                                                                                 cytostatic; neuroprotective; antiparkinsonian; hepatotropic; cerebroprotective; antiinflammatory; nootropic; vasotropic; arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease; Parkinson's; Crohn's; gene therapy; human.
                                                                                                                                                                                                                protein; IRAP; antiarteriosclerotic;
                                                                                                                                                               Human immune response associated protein IRAP-23 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 382.5; DB 8; 33.9%; Pred. No. 4.4e-24; ive 60; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Elliott VS, Hafalia A
Marquis JP, Chawla NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 23; 207pp; English
                      ADK98560 standard; protein; 565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-2002; 2002US-0410178P.
13-SEP-2002; 2002US-0410571P.
18-OCT-2002; 2002US-0419906P.
25-OCT-2002; 2002US-0421445P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-2003; 2003WO-US026988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0407561P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Swarnakar A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lindquist EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-239178/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADK98595.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004020593-A2
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                    03-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 101;
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                                                                       ADK98560;
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ADK98560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to new immunoglobulin superfamily proteins (IGSFP). The polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing treating or preventing disorders associated with aberrant expression of IGSFP, particularly cell proliferative, e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, parcxysmal cocturnal haemoglobiuntia, polycythaemia vera, psoriasis, primary thrombocytopenia or cancers including leukaemia, lymphoma, sarcoma or myeloma, and autoimmune or inflammatory disorders, e.g. acquired myproiditis, contact dermatitis, languages, asthma, asthma, autoimmune thyroiditis, contact dermatitis, coln's disease, diabetes mellitus, chroiditis, contact dermatitis, coln's disease, diabetes mellitus, contact dermatitis, syndrome, syndrome, multiple sclarosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arbitists, Sjogren's syndrome, uveitis, trauma, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of IGSPP protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KRYNLOIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEFTLFVYEQLQEPQVTMKSVKVSENFSCNITLMCSVKGAEKSVLYSWTPREPHASESNG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human immunoglobulin superfamily proteins and polynucleotides, useful for diagnosing, treating or preventing disorders with aberrant IGSFP expression, such as autoimmune, inflammatory or cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFFLLVLILSS-----VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 OHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA
                                                                                                                                                                                                                                                                                                 velu K, Warren BA, Tang YT, Duggan BM;
Honchell CD, Burford N, Forsythe IJ, Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 129-130; 145pp; English
                                                                                             12-MAR-2001; 2001US-0275249P.
31-AUG-2001; 2001US-0316810P.
21-SEP-2001; 2001US-033977P.
25-OCT-2001; 2001US-0343880P.
                                                       12-MAR-2002; 2002WO-US009052
                                                                                                                                                                                                                                                                                                   Thangavelu K,
                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                                             Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-723340/78.
N-PSDB; ABS76363.
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Matches 101; Conserv
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          19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                    Mason PM;
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Hafalia AJA, Richardson awla NK, Khare R, Becha

88

37;

Length 565; Indels

셤 8 셤 ò g ઠે g 8 Length 610;

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The present invention relates to a new method for screening for susceptibility to a systemic autoimmune disorder. The method comprises screening for at least one mutation within the systemic lupus crythemacosus (SLE)-1B loci. Screening for susceptibility to autoimmune disorders such as systemic lupus erythematosus involves screening for at least one mutation in a gene or genes with the SLE-1B loci such as a gene cancidar signalling lymphocyte activation molecule (SLAM), lymphocyte activation molecule (SLAM), lymphocyte antigen (Ly)-9, 284 (a natural killer cell receptor), CD48, CD64, LX108, CS1, DEDD, NITI, upstream transcription factor (USF), GOLGA4. The method cof the invention is useful for treating SLE and involves administering a construct comprising a wild-type sequence encoding any one of the above mentioned genes. Gene therapy also involves the use of antisense constructs or ribozymes directed against the above mentioned genes for treating SLE. Note: The present protein sequence represents a human creating SLE. Note: The present protein sequence represents a human content of the mediate a break in immune tolerance. This sequence is shown the sequence listing but is not further defined in the specification
                                                                                                         144 BEFTLEVYEQLQEPQVTWKSVKVSENFSCNITLMCSVKGAEKSVLYSWTPREPHASESNG 203
---GEE 174
                                                                                 GNVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for susceptibility to systemic autoimmune disorder by screening for a mutation within the systemic lupus erythematosus-1B loci.
                                                                                                                                                                                          263 EPVTLPLALPACRDTEKVVWLFNTSIISKERBEAATADPLI-----KSRDPYKNRVW 314
                                                                                                                                                                  232 MFFLLVLILSS-----VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; systemic lupus erythematosus 1B; SLE-1B; dermatological; antiinflammatory; immunosuppressive; systemic autoimmune disorder; aignalling lymphocyte activation molecule; SLAM; lymphocyte antigen 9; Ly-9; 2B4; natural killer cell receptor; CD48; CD84; LY108; CS1; DEDD; NIT1; upstream transcription factor 1; USF 1; GOLGA4; immune tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein sequence #3, related to isolation of genes within SLE-1B.
KRYNLQIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2001; 2001WO-US016051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2000; 2000US-0204963P.
21-SEP-2000; 2000US-0234457P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakeland EK, Wandstrat A,
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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122
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Sequence 610 AA;

58 FARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 112 KRYNLQIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEE 174 YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121 GNVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLA 231 61 57 232 MFFLLVLILSS-----VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279 232 EPVTLPLALPACRDTEKVVWLFNTSIISKEREEAATADPLI-----KSRDPYKNRVW 283 3 OHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA QTSLLFLLMGLR----ASGKDSAPTVVSGILGGSVTLPLNISVDTEIENVIWIGPKNALA Gaps 37; Indels Query Match 22.6%; Score 382.5; DB 5; Best Local Similarity 33.9%; Pred. No. 4.9e-24; Matches 101; Conservative 60; Mismatches 100; ~ 62 122 175 Search ð 셤 ð d δ 셤 à d ò a

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Sequence 7327, App
Sequence 7327, App
Sequence 7325, Ap
Sequence 8, Appli
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Sequence 6
Sequence 6
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1: /cgn2_6/prodata/l/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/l/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/l/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/l/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/l/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/l/iaa/PCTUS COMB.pep:*
5.1.6
Compugen Ltd
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US-09-949-016-6907
US-09-949-016-6907
US-08-18-8
US-08-18-8
US-08-199-955-8
US-08-880-875-2
US-08-462-738-2
US-08-462-738-2
US-08-462-738-2
US-09-199-955-2
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US-09-199-955-2
US-09-199-955-4
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GenCore version
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1696
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Sequence 2, Appl	Sequence 12, App	Sequence 12, App	Sequence 12, App	Seguence 12, App	Sequence 4353, A	Sequence 1, Appl:	Sequence 320, Ap	Sequence 320, Ap	Sequence 320, Ap	Sequence 320, App	Sequence 320, Ap	Sequence 320, Ap	_	Sequence 320, Ap	_	Sequence 20, Api	Sequence 6, Appl
US-09-369-248A-2	US-08-348-792-12	US-08-462-738-12	US-09-199-955-12	US-08-880-875-12	US-09-513-999C-4353	US-09-435-956A-1	US-09-907-794A-320	US-09-905-125A-320	US-09-902-775A-320	US-09-906-700-320	US-09-903-603A-320	US-09-904-920A-320	US-09-909-064-320	US-09-905-381A-320	US-09-906-618-320	US-09-919-172-20	US-08-466-465-6
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285	329	329	329	329	144	458	450	450	450	450	450	450	450	450	450	518	351
9.8	9.8	9.6	9.6	8.6	9.5	8.3	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1	8.1
166.5	165.5	165.5	165.5	165.5	161	140.5	138	138	138	138	138	138	138	138	138	137.5	137
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/941,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-08
SEQ ID NOS: 207012
SOFTWARE: FASLSEQ for Windows Version 4.0
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100.0%; Pred. No. 3.5e-166;
iive 0; Mismatches 0;
                 Sequence 6428, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 328; Conservative
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US-09-949-016-6428
US-09-949-016-6428
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301 EVQFADKMGKASTQDSKPPGTSSYEIVI 328

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US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
301 EVQPADKMGKASTQDSKPPGTSSYEIVI 328
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ER FILING DATE: 1997-03-07

ER APPLICATION NUMBER: 60/047,600

ER APPLICATION NUMBER: 60/047,615

ER APPLICATION NUMBER: 60/047,597

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,502

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,502

ER RILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,613

ER APPLICATION NUMBER: 60/047,617

ER RAPLICATION NUMBER: 60/047,503

ER PILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,592

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,592

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ER APPLICATION NUMBER: 60/047,592

ER FILING DATE: 1997-05-23

ER PELING DATE: 1997-05-23

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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,598
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,613
R FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-10
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER RPLING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,893
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,630
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,313
R FILING DATE: 1997-04-11
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R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,879 APPLICATION NUMBER: 60/056,894 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,911 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,880 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,864 SARLIER APPLICATION NUMBER: 60/056,631 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 1997-08-22 1997-08-22 1997-08-22 1997-08-22 FILING DATE: 1997-08-22 1997-08-FILING DATE: LING DATE: FILING DATE: LING DATE: EARLIER EARLIER EARLIER EARLIER

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Sequence 72.7. Application US/09949016
; Sequence 72.7. Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VANTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: 2000-0-04-14, 755
    PRIOR APPLICATION NUMBER: 60/241, 756
    PRIOR PLING DATE: 2000-10-03
    PRIOR SPLICATION NUMBER: 60/231, 498
    PRIOR FILING DATE: 2000-10-03
    PRIOR PLING DATE: 2000-10-03
    PRIOR SPLICATION NUMBER: 60/231, 498
    PRIOR FILING DATE: 2000-10-03
    PRIOR PRING DATE: 2000-10-03
    PRIOR PRING DATE: 2000-10-03
    PRIOR PRINGE DATE: 2000-10-03

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TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
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Best Local Similarity 100.
Matches 328; Conservative
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ORGANISM: Human
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US-09-949-016-6907
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US-09-949-016-7327
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Best Local Similarity 100.0%; Pred. No. 3.5e-166;
Matches 328; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-66
EARLIER FILING DATE: 1997-06-66
EARLIER FILING DATE: 1997-06-65
EARLIER FILING DATE: 1997-06-65
EARLIER FILING DATE: 1997-06-65
EARLIER PILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                R APPLICATION NUMBER: 60/047,586

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,590

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,594

R APPLICATION NUMBER: 60/047,594

R APPLICATION NUMBER: 60/047,593

R APPLICATION NUMBER: 60/047,593

R APPLICATION NUMBER: 60/047,514

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,514

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,576

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,576

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,670

R FILING DATE: 1997-04-12

R APPLICATION NUMBER: 60/056,664

R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,664

R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,876

R RILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,876

R RILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,876

R RILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,875

R RILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,875

R R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,875

R R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,875

R R FILING DATE: 1997-08-22

R R FILING DATE: 1997-08-22

R R PLING DATE: 1997-08-22
         R APPLICATION NUMBER: 60/057,761
R FILING DATE: 1997.08-22
R FILING DATE: 1997.08-22
R FILING DATE: 1997.05-23
R FILING DATE: 1997.05-23
R FILING DATE: 1997.05-23
R PILING DATE: 1997.05-23
R APPLICATION NUMBER: 60/047,588
R PILING DATE: 1997.05-23
R FILING DATE: 1997.05-23
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CLASSIFICATION: 350
ATTORNEY/AGENTINN: DAME:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION: INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: California
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                                                                                                                               Query Match
Best Local Similarity
Matches 85; Conserv
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                            ; ORGANISM: Human
US-09-949-016-7325
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US-08-348-792-8
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                                                        APPLICANT: VENTER, AC. VENTER,
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: O. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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| SEC -FWPFLVIIVILSALFLGTLACFCVWRRKRKEKQSETSPKEFLTIYEDVKDLKTRRNHEQ 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SVAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 TTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW----SPLGEE 174
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23.6%; Pred. No. 1e-14;
ive 65; Mismatches 142; Indels
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CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-04-175
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTESEQ for Windows Version 4.0
SEQ ID NO 7325
6907, Application US/09949016
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-6907
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US-09-949-016-7325
                                          Patent No. 68123
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59 SVAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPY 118
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                                                                                                                                                                       87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: WITHER OF VINENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
CORRESPONDENCE ADDRESS:
     Length 391;
13.4%; Score 227; DB 4; Length 39 ilarity 23.6%; Pred. No. 1.1e-14; Conservative 65; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
DATHORNIN: S30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: DNAX Research Institute
901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5576423
GENERAL INFORMATION:
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71 YLE-----NITLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 OSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 YTCTAQNPVSNNSDSISARQLCADIAMGFRTH------HTGLLSVLAMFFLLVLILS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 SVFLFRLFKRR-----QDAASKKTIYTYIMASR----NTQPAE---SRIYDEILQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| : || : || : 232 -----LRRRGKTNHYQTTVEKKSLTIYAQVQKPGPLQKKLDSFPAQDPCTTIY--VAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 IGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 70
                                                                                                                                                                                                                                                                          33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVHRN
                                                                                                                                                                                                               Gaps
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APPLICANT: Aversa, Gregorio

APPLICANT: Cocks, Benjamin G.

APPLICANT: Cocks, Benjamin G.

APPLICANT: de Vries, Jan E.

TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL

TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                              DB 2; Length 307;
1.9e-11;
                                                                                                                                              ; Score 194; DB 2; Length 30; Pred. No. 1.9e-11; 54; Mismatches 112; Indels
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CITY: Palo Alto
COUTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Paloppy disk
COMPUTER: Paloppy disk
COMPUTER: Paloppy disk
COMPUTER: Palopy dis
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APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/348,792
APPLICATION DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE / DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/199,955 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 SKVLPSKEEPVN--TVYSEV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 California Avenue
                                                                                                                                                  11.4%;
                                                                                                                        Query Match
Best Local Similarity 23.0.
Best Local Conservative
''^a
                         TOPOLOGY: linear
MOLECULE TYPE: protein
amino acid
                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                       ; MOLECULE TO
US-08-462-738-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
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                                                                                                                                                                                                                      33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVHRN 80
                                                                                                                                                           Gaps
                                                                                                                                                           78;
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GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Canay, Cria-chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Ge Vries, Jan E.
TITLE OF INVENTION: FURLFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURPACE ANTIGENS, PROTEINS AND ANTIBODIES
                                                                                              Length 307;
                                                                                       11.4%; Score 194; DB 1; Length 30
23.8%; Pred. No. 1.9e-11;
ive 54; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REFERENCE/DOCKET NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELEPHONE: 415-652-9196
TELEPHONE: 415-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 8, Application US/08462738
; Patent No. 5977303
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                                                                                                                              Best Local Similarity 23.8*
Matches 76; Conservative
         MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
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                ; MOLECULE 13
US-08-348-792-8
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                                                                                                 Query Match
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                           81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 SVFLFRLFKRR-----QDAASKKTIYTYIMASR-----NTQPAE---SRIYDEILQ 284
                                                                                                                                                                                                                    33 LGESVIFP-----VNIQEPRQVKIIAWISKI-----SVAYVIPGDSEIAPVVIVHRN 80
                                                                                                                                                                                                                                            11 LGSKVLLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 70
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                      78;
                                                                                                                                                  11.4%; Score 194; DB 3; Length 307;
23.8%; Pred. No. 1.9e-11;
ive 54; Mismatches 112; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"OWDITER: IBM PC COMPATIBLE
""" FC-DOS/MS-DOS
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901 California Avenue
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Patent No. 6399065
                                                : 307 amino acids amino acids
                                                                                                                                                   Query Match
Best Local Similarity 23.89
Matches 76; Conservative
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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CITY: Palo Alto
STATE: California
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US-09-199-955-8
                                                    LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 YTCTAQNPVSNNSDSISARQLÇADIAMGFRTH------HTGLLSVLAMFFLLVLILS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
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Patent No. 5576423

GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: FURIFIED GENES ENCODING MANMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
CORRESPONDENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESSES.
ADDRESSES: DAXX Research Institute
                                                                                                                                                                                                                                                                                                                                                Length 307;
                                                                                                                                                                                                                                                                                                                                              Query Match 11.4%; Score 194; DB 3; Length 30
Best Local Similarity 23.8%; Pred. No. 1.9e-11;
Matches 76; Conservative 54; Mismatches 112; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
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901 California Avenue
                                DX0436K
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REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
        34,090
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ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1994
                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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99 YLE-----NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLXEQVSTPEIK 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 YTCTAQNPVSNNSDSISARQLCADIAMGFRTH-----HTGLLSVLAMFFLLVLILS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 LGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
APPLICANT: Cocke, Benjamin G.
TITLE OF INVENTION: BURFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 194; DB 2; Length 335; 23.8%; Pred. No. 2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
                                                                                                                                                                                                                                                                                                                                                                                                            54; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 TEPVPESVQETNSITVYASV 330
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX.
TELECOMMUNICATION:
TELEPHONE: 415-852-9196
                                                                                                                       TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          LENGTH: 335 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            76; Conservative
                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
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Best Local Similarity
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STATE: Californ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-199-955-2
                                                                                                                                                                                                                                                                                                          US-08-462-738-2
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                                                                                                                                                                                                                                                                                                                                                             78; Gaps
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Sequence 2, Application US/08462738

Sequence 2, Application US/08462738

Sequence 2, Application US/08462738

SERICANT No. 5977303

APPLICANT: Chang, Chia-Chun J.

APPLICANT: Chang, Chia-Chun J.

APPLICANT: Cock, Benjamin G.

APPLICANT: Ge Vries, Jan E.

TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL

TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES

UNMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                          11.4%; Score 194; DB 1; Length 335; 23.8%; Pred. No. 2.2e-11; tive 54; Mismatches 112; Indels
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ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PACHON PC-DOS/MS-DOS
SOFTWARE: PACHTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUIENCE CHARACTERISTICS:
LENGTH: 335 amino acids
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APPLICATION NUMBER: US 0
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 23.8% Matches 76; Conservative
            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                : 335 amino acids
amino acid
                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
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81 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 138
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; APPLICANT: Young, Paul; APPLICANT: When Particle of INVENTION: Molecule; TITLE OF INVENTION: Molecule; TITLE OF INVENTION: Molecule; FILE REFERENCE: PF448P1; CURRENT APPLICATION NUMBER: US/09/369,248A; CURRENT FILING DATE: 1999-08-05; PRIOR FILING DATE: 1999-00-06; PRIOR FILING DATE: 1998-03-19; PRIOR APPLICATION NUMBER: 60/078,572; PRIOR PLING DATE: 1998-03-19; PRIOR PLING DATE: 1998-03-19; PRIOR PLING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 LGSKVLLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 YICTVSNPISNNSQTFSPWPGC-----RIDPSETKPWAVYAGLIGGVIMILIMVVILQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.4%; Score 194; DB 3; Length 335; 23.8%; Pred. No. 2.2e-11; Live 54; Mismatches 112; Indels
Filians
CLASSIFICATION: ---
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/481,777
APPLICATION NUMBER: US 08/481,777
TING DATE: 07-UN-1995
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                                                                                                                   FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/348,
FILING DATE: 02-DEC-1994
ATTONNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFRENCE/DOCKET NUMBER: DX04:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.00.
Terror 76; Conservative
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SOFTWARE: Patentin Ver. SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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ORGANISM: Homo sapiens
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US-09-369-248A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 -----LRRRGKTNHYQTTVEKKSLTIYAQVQKPGPLQKKLDSFPAQDPCTTIY--VAA 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
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GENERAL INFORMATION:
APPLICANT: Average Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: We Vries, Jan E.
TITLE OF INVENTION: FUBLIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 194; DB 3; Length 33 23.8%; Pred. No. 2.2e-11; tive 54; Mismatches 112; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
                        APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-1200
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CORRESPONDENCES.
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
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                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 335 anthro acids TYPE: amino acid TOPOLOGY: linear
       05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 23.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94134-1164
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-09-199-955-2
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US-08-880-875-2
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Matches
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                                                                                                                                                                                                                                                          33 IGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN 80
                                                                      Query Match
11.4%; Score 194; DB 4; Length 335;
Best Local Similarity 23.8%; Pred. No. 2.2e-11;
Matches 76; Conservative 54; Mismatches 112; Indels
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION UMBER: US/09/227,357
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EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER PELLING DATE: 1990-01-07
EARLIER PELLING DATE: 1997-07-07
EARLIER PELLING DATE: 1997-07-08
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R APPLICATION NUMBER: 60/051,916

R FILING DATE: 1997-07-08

R PILING DATE: 1997-07-08

R PAPLICATION NUMBER: 60/051,930

R PAPLICATION NUMBER: 60/051,918
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FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,932
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FILING DATE: 1997-07-08
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PLICATION NUMBER: 60/051,919
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FILING DATE: 1997-07-08
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US-09-369-248A-3
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60 VAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYT 119
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER PILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER PILING DATE: 1997-08-18
EARLIER PILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER PILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                       FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,947
FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
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SEQ ID NO 192
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Matches 44; Conserv
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LOCATION: (138
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us-09-882-171-483.rapb

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Sequence 483, App
Sequence 483, App
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(egn2_6)prodata/2/pubpaa/US07_PUBCOMB.pep:*

(egn2_6)prodata/2/pubpaa/US07_NEW_PUB.pep:*

(egn2_6)prodata/2/pubpaa/US06_NEW_PUB.pep:*

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(egn2_6)prodata/2/pubpaa/US07_NEW_PUB.pep:*

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(egn2_6)prodata/2/pubpaa/US08_NEW_PUB.pep:*

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(egn2_6)prodata/2/pubpaa/US08_PUBCOMB.pep:*

(egn2_6)prodata/2/pubpaa/US08_PUBCOMB.pep:*

(egn2_6)prodata/2/pubpaa/US08_PUBCOMB.pep:*

(egn2_6)prodata/2/pubpaa/US09_NEW_PUB.pep:*

(egn2_6)prodata/2/pubpaa/US106_PUBCOMB.pep:*

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Compugen Ltd.
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US-10-445-523-30
US-09-809-391-483
US-09-882-171-483
US-10-164-861-483
US-10-104-861-483
US-10-104-943-7
US-10-104-943-7
US-10-328-538-2
US-10-328-538-2
US-10-328-538-2
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  OM protein - protein search, using sw model
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1696
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Maximum DB seq length: 200000000
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Sequence 88, Appl Sequence 90, Appl Sequence 91, Appl Sequence 31, Appl Sequence 25, Appl Sequence 253, App Sequence 253, App	equence 253 equence 253 equence 253 equence 253 Sequence 25 Sequence 25 Sequence 25
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ALIGNMENTS

RESULT 1		
US-10-104-943-4		
; Sequence 4, Application US/10104943		
; Publication No. US20030092017A1		
; GENERAL INFORMATION:		
, APPLICANT: Bristol-Myers Squibb Company		
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL IMMUNOGLOBULIN SUPERFAMILY MEMBE.	ERFAMILY	MEMBE.
; TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF		
; FILE REFERENCE: D0135 NP		
; CURRENT APPLICATION NUMBER: US/10/104,943		
; CURRENT FILING DATE: 2002-03-22		
; PRIOR APPLICATION NUMBER: US 60/278,037		
; PRIOR FILING DATE: 2001-03-22		
; PRIOR APPLICATION NUMBER: US 60/281,223		
; PRIOR FILING DATE: 2001-04-03		
; NUMBER OF SEQ ID NOS: 129		
; SOFTWARE: PatentIn version 3.0		
; SEQ ID NO 4		
; LENGTH: 328		
; TYPE: PRT		
; ORGANISM: Homo sapiens US-10-104-943-4		
99.98;		
Best Local Similarity 100.0%; Fred. No. 26-144; Matches 328: Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy 1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV 60		
Db 1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV 60		
Qy 61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120		
Db 61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120		
Qy 121 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI 180	1 180	

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SEQ ID NO 483
LENGTH: 329
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                                             FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
                                                                          SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
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100.0%; Pred. No. 2e-144;
live 0; Mismatches 0;
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US-10-436-523-30
Sequence 30, Application US/10436523
Publication No. US20030180888A1
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 328; Conservative
                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-09-809-391-483
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Sequence 483, Application US/09809391 Publication No. US20030049618A1 GENERAL INFORMATION: APPLICANT: Ruben et al.

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241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
241 SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSV
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0
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TITLE OF INVENTION: 186 Human Secreted proteins
PILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.9%; Score 1695; DB 10;
100.0%; Pred. No. 2.1e-144;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (329)
OTHER INFORMATION: Xaa equals stop translation
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TITLE OF INVENTION: 186 Human Secreted prote:
FILE REFERENCE: PZ002P2
CURRENT PPLICATION NUMBER: US/09/882,171
CURRENT PELING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
PRIOR PRIOR DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 328, Conservative
                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: SITE
LOCATION: (329)
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R APPLICATION NUMBER: 60/043,672 R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/043,315 R FILING DATE: 1997-04-11 R APPLICATION NUMBER: 60/048,974 R FILING DATE: 1997-06-06 DR APPLICATION NUMBER: 60/043,580
DR FILING DATE: 1997-04-11
DR APLICATION NUMBER: 60/043,588
DR PLING DATE: 1997-04-11
DR APPLICATION NUMBER: 60/043,314
DR PLING DATE: 1997-04-11
DR APPLICATION NUMBER: 60/043,314
DR PILING DATE: 1997-04-11
DR APPLICATION NUMBER: 60/043,569
DR FILING DATE: 1997-04-11
OR APPLICATION NUMBER: 60/043,511
OR PILING DATE: 1997-04-11
OR PLING DATE: 1997-04-11 R FILING DATE: 1997-04-11
R PAPLICATION NUMBER: 60/043,674
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,669
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,617

R APPLICATION NUMBER: 60/047,618

R APPLICATION NUMBER: 60/047,618

R FILING DATE: 1997-05-23

R R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,503 PILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23 FILING DATE: 1997-05-23
APPLICATION WINBER: 60/047,596
APPLICATION DATE: 1997-05-23
APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,600 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,615 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,597 APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-03-07 APPLICATION NUMBER: 60/040,163 FILING DATE: 1997-03-07 APPLICATION NUMBER: 60/047,502 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,583 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,587 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 PRIOR
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R APPLICATION NUMBER: 60/056,888
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,879
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,994
R FILING DATE: 1997-08-22 R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/057,761 R FILING DATE: 1997-08-22
A PAPLICATION NUMBER: 60/056,877
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,893
R FILING DATE: 1997-08-22 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,595
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,599
FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION WUMBER: 60/047,589 ELING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 FILING DATE: 1997-04-11 APPLICATION VUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/047,588 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,585 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,614 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22
APPLICATION UNDBER: 60/056,872
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,874 APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 1997-05-23 FILING DATE: 1997-08-22 PRIOR
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                                                                                                                                                                                                                                                                       Length 329;
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APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
APPLICANT: TRAN, Y. TOM, DUGGAN, Brendan M.;
APPLICANT: TRAN, UYEN K.; BAUGHN, Mariah R.;
APPLICANT: HONCHELL, Cynthia D.; BURFORD, Neil;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
APPLICANT: MASON, Patricia M.
TITLE OF INTENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0925 USN
                                                                                                                                                                                                                                                                         99.9%; Score 1695; DB 15; 100.0%; Pred. No. 2.1e-144; tive 0; Mismatches 0;
                                                                                                                                                  NAME/KEY: SITE
LOCATION: (329)
COTHER INFORMATION: Xaa equals stop translation
US-10-164-861-483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVQFADKMGKASTQDSKPPGTSSYEIVI 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/10471449; Publication No. US20040097711A1; GENERAL INFORMATION:
                   PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 328; Conservative
NUMBER OF SEQ ID NOS: 757
                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                 SOFTWARE: Pat
SEQ ID NO 483
LENGTH: 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 483, Application US/10164861

Publication No. US20030225248A1

Sequence 483, Application US/10164861

Publication No. US20030225248A1

APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERRENCE: PZ00221

CURRENT FILING DATE: 2002-06-10

PRIOR PILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 EVOFADKMGKASTODSKPPGTSSYEIVI 328
              PRIOR APPLICATION NUMBER: 60/043,670
PRIOR FILING DATE: 1997-04-11
PRIOR PILING DATE: 1997-04-11
PRIOR PELING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/056,664
PRIOR PILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,816
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-06-26
PRIOR PELING DATE: 1997-06-26
PRIOR PELING DATE: 1997-06-66
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-22
PRIOR PELING DATE: 1997-08-05
PRIOR PELING DATE: 1997-08-05
PRIOR PELING DATE: 1997-08-05
FILING DATE: 1997-05-23
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Sequence 11, Application US/09860836B

Publication No. US20030054002A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WANDSTRADT, AMY
APPLICANT: WANDSTRADT, AMY
TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK
TITLE OF INVENTION: IN IMMUNE TOLERANCE
TITLE OF INVENTION: IN IMMUNE TOLERANCE
TITLE OF INVENTION: IN UNMER: US/09/860,836B
CURRENT APPLICATION NUMBER: US/09/860,836B
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/204,963
PRIOR PILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 37

SOFTWARE PATENTING VOS: 37

SOFTWARE PATENTING VOS: 2.1
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                                                                                                                                                                                                                                                                                                                                   FARPKEN-----VTIMVKSYLGRLDITKWSYSLCISNLTLNDAGSYKAQINQRNFEVTTE 143
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                                                                                                                                                                                                                                                                                                        62 YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
                                                                                                                                                                                                                                                                                                                                                                                               KRYNLQIYRRLGKPKIT-QSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEE 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 MFFLLVLILSS-----VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                                                                                                                                                    3 QHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTS-KTSVA
                                                                                                                                                                                                                                           Indels 37;
                                                                                                                                                                           37;
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                                                                                                                            DB 15; Length 551;
                                                                                                                                                                           Indels
                                                                                                                          Query Match 22.6%; Score 382.5; DB 15; Best Local Similarity 33.9%; Pred. No. 1.3e-25; Matches 101; Conservative 60; Mismatches 100;
                                  NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No: 7500099CD1
US-10-471-449-8
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapien
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US-09-860-836B-11
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LENGTH: 610
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Sequence 7, Application US/10104943
; Beduence 7, Application US/10104943
; Publication No. U32033092017A1
; General Information.
; Title OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL IMMUNOCLOBULIN SUPERFAMILY MEMBER
; TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF
; TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0135 NP
; CURRENT APPLICATION NUMBER: US/10/104,943
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/278,037
; PRIOR PILING DATE: 2001-04-03
; PRIOR PILING DATE: 2001-04-03
; NUMBER OF ESQ ID NOS: 129
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7.
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US-10-612-2
US-10-612-2
Sequence 2, Application US/10310612
; Sequence 2, Application US/10310612
; Sequence 2, Experimental Company 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
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                                                                                             232 MFFLLVLILSS------VFLFR---LFKRRQDAASKKTIYTYIMASRNTQPAESRIY 279
                                                                                                                                              233 FFLLVLILSS-----VFLFR---LFKRRQDAASKKTIYTYMASRNTQPAESRIY 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 QTSLLFLLMGLR----ASGKDSAPTVVSGILGGSVTLPLNISVDTEIENVIWIGPKNALA
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22.1%; Score 374; DB 14; Length 654
Best Local Similarity 33.0%; Pred. No. 9.9e-25;
Matches 98; Conservative 59; Mismatches 104; Indels
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US-10-310-612-2
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ORGANISM: Homo sapiens
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US-10-436-523-76
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TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
TITLE OF INVENTION: that express Ly-9
FILE REPERBNCE: HYS-68CP
CURRENT APPLICATION NUMBER: US/10/328,538
CURRENT FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                            KRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEEG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 EEFTLFVYEQLQEPQVTMKSVKVSENFCNITLMCSVKGAEKSVLYSWTPREPHASESNGG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLAM 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVLQIFQTPEDQELTYTCTAQNPVSNNSD-SISARQLCAD--IAMGFRTHHTGLLSVLAM 232
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                                                                                                                                                                                                                                                                                               62 YVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTT 121
                                                                                                                                                   3 QHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA 61
                                                                                                                                                                                                                   33 QTSLLFLLMGLR----ASGKDSAPTVVSGILGGSVTLPLNISVDTEIENVIWIGPKNALA 88
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Length 654;
22.1%; Score 374; DB 16; Length 6 ilarity 33.0%; Pred. No. 9.9e-25; Conservative 59; Mismatches 104; Indels
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US-10-328-538-2
'Sequence 2, Application US/10328538
'Publication No. US20040109863A1
'GENERAL INFORMATION:
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Best Local Similarity 33.09
Matches 98; Conservative
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ORGANISM: Homo sapiens
   Query Match
Best Local Similarity
Matches 98; Conserva
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US-10-328-538-2
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RESULT 11

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APPLICANT: No. US20030124575Alartis AG
APPLICANT: No. US20030124575Alartis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Phares, William
APPLICANT: Werner, Gudrun
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; Sequence 76, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF;
; TILE REFERENCE: 7853-244-999
; CURRENT APPLICATION UNMBER: US/10/436,523
; CURRENT FILING DATE: 2003-05-12
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR FILING DATE: 2000-11-3
; NUMBER OF SEQ ID NOS: 100
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                                                                                                        APPLICANT: NO. US200301245/SAlartis As
APPLICANT: NO. US200301245/SAlartis Erfindungen Verwaltung
APPLICANT: Phares, William
APPLICANT: Wenner, Gudrun
APPLICANT: Jartiz, Markus
APPLICANT: Lapp, Hilmar
APPLICANT: Lapp, Hilmar
APPLICANT: Lapp, Hilmar
TITLE OF INVENTION: Organic Compounds
FILE REFERENCE: 4.31347 PCT
CURRENT APPLICATION NUMBER: US/0/220,946
CURRENT FILING DATE: 2002-99-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR PLILING DATE: 2000-05-18
PRIOR PLILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 22
SUFTWARE: PastSEQ for Windows Version 4.0
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Sequence 18, Application US/10220946 Publication No. US20030124575A1 GENERAL INFORMATION:
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US-10-220-946-18
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60 VAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYT 119
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                                                          EGNVLQIFQTPEDQELTYTCTAQNPVSN-NSDSISARQLCADIAMGFRTHHTG---LLSV 229
                                                                                                                                   7 WILLLCL-----QTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTS
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                                     TTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGE----
                                                                                                                                                                                                                                                                                                              Sequence 88, Application US/10436523
; Sequence 88, Application US/10436523
; Publication No. US20033180888A1
; CENERAL INFORMATION:
    APPLICANT: Fraser, Christopher C.
    TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICATION NUMBER: US/10/436,523
; PRIOR PILING DATE: 2001-11-20
; PRIOR FILING DATE: 2001-11-03
; RIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Version 3.1
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; Publication No. US20030180888A1
; GENERAL INFORMATION:
   APPLICANT: Fraser, Christopher C.
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-999
; CURRENT APPLICANT ONUMEE: 2003-05-12
; CURRENT PILING DATE: 2003-05-12
; FRIOR APPLICATION NUMBER: US/10/007,303
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1 Similarity 31.7%; Pred. No. 7.2e-25;
91; Conservative 55; Mismatches 119;
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US-10-436-523-88
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Best Local Similarity
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US-10-436-523-89
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US-10-436-523-88
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                                                                                                                                       22.0%; Score 373; DB 14; Length 289; 32.1%; Pred. No. 3.9e-25;
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                                                                                                                                                                             54; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kingsman, Susan Mary
APPLICANT: Kingsman, Susan Mary
APPLICANT: Kinge, David
TITLE OF INVENTION: ANALYSIS METHOD
TITLE OF INVENTION: ANALYSIS METHOD
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR PILING DATE: 2002-04-08
PRIOR PLILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Christopher Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 131, Application US/10170385 Publication No. US20030203372A1 GENERAL INFORMATION:
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Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mundy, Christopher R
Kan, On
Harris, Robert Alan
         SOFTWARE: PatentIn version 3.1
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Best Local Similarity 32.1%
Matches 92; Conservative
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                                                                                  ORGANISM: Homo sapiens
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SEQ ID NO 131
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                                                                                                      US-10-436-523-76
                           SEQ ID NO 76
LENGTH: 289
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                  6 WILLILLIQEGSQRRLWRWCGSEE-----VVAVLQESISLPLEIPPDEEVENIIWSSHKS 60
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                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                         Query Match 21.8%; Score 370; DB 14; Length 289; Best Local Similarity 31.7%; Pred. No. 7.2e-25; Matches 91; Conservative 55; Mismatches 119; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 LAMFFLLVLILSSVFLFRLFKRRODAASKKTIYTYIMASRNTQPAES 276
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; PRIOR FILING DATE: 2001-11-20; PRIOR APPLICATION NUMBER: 09/706,167; PRIOR FILING DATE: 2000-11-03; NUMBER OF SEQ ID NOS: 100; SOFTWARE: Patentin version 3.1; SEQ ID NO 89; LENGTH: 289; TYPE: PRT (CREATER PRT); ORGANISM: Homo sapiens US-10-436-523-89
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Search completed: February 4, 2005, 12:32:17 Job time : 110.42 secs

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GenCore version 5.1.6
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2005, 12:03:57 ; Search time 31.7784 Seconds	(without alignments)	996.126 Million cell updates/sec
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US-09-882-171-483 1696 1 MAQHHLWILLLCLQTWPEAA.......KASTQDSKPPGTSSYEIVIX 329

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Regult		Ouerv				
No.	Score	Match	모	DB	ID	Description
	336	19.8	629	7	A46500	Ly-9.2 antigen - m
8	194	11.4	335	N	S58892	
М	180	10.6	240	~	801299	OX-45 membrane gly
4	179.5	10.6	240	~	JL0143	œ.
ß	164	7.6	398	7	I49443	₹*
9	143.5	8.5	521	7	S34338	
7		8.4	458	Н	WMMSR1	
80		8.4	521	N	JC1508	>
6		8.3	347	~	S41638	T-cell surface gly
10	139.5	8.2	458	N	JC1509	biliary glycoprote
	137.5	8.1	518	7	JC4024	poliovirus recepto
12	137	8.1	351	Н	RWHUC2	T-cell surface gly
13	135.5	8.0	702	~	A36319	carcinoembryonic a
14	134.5		417	, -1	RWHUPA	poliovirus recepto
15			344	7	A27681	nonspecific cross-
16	127.5		344	7	B28967	T-cell surface gly
17			392	٦	RWHUPD	poliovirus recepto
18	125	7.4	338	7	JC4776	limbic-system-asso
19	124.5	7.3	519	7	A44783	ecto-ATPase precur
50	123.5	7.3	417	~	A44194	
21	122.5			~	JH0395	biliary glycoprote
22	122.5			~	JH0396	
23	122.5	7.2		7	JH0394	biliary glycoprote
24	122.5			~	C30127	transmembrane carc
25				н	A32164	biliary glycoprote
56			338	~	JC1238	opioid-binding pro
27		7.2		~	I49585	CD2 antigen protei
28	121.5	7.2		N	803199	
29	121.5	7.2	345	N	JC1239	opioid-binding pro

carcinoembryonic a opioid binding cel 50K glycoprotein p	neurotrimin - rat pregnancy-specific pregnancy-specific	pregnancy specific biliary glycoprote pregnancy specific	pregnancy-specific pregnancy-specific pregnancy-specific pregnancy-specific	pregnancy, specific pregnancy-specific pregnancy-specific pregnancy-specific
A55811 JC4025 JC5519	156551 A28277 A33258	B33258 JC1511 JC4123	D43354 C43354 E43354	A35964 A35341 A27658
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ALIGNMENTS

RESULT 1 A46500 Ly-9.2 antigen - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Jun-1993 #sequence_revision	RESULT 1 A46500 L1-9.2 antigen - mouse C;Species: Mus musculus (house mouse) C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A45500 R;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, J J. Immunol. 149, 1636-1641, 1992 A;Title: Isolation and characterization of cDNA clones A;Reference number: A46500; MUID:92373005; PMID:1506686	C;Accession: A46500 K;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A. J. Immunol. 149, 1636-1641, 1992 A;Title: Isolation and characterization of cDNA clones for mouse Ly-9. A;Reference number: A46500; MUID:92373005; PMID:1506686
A,Accession: A46500 A,Status: preliminary A,Molecule type: mRNA, protein	
A, Cross-references: GB.M84412; NID:g1: A, Experimental source: C57BL/6 A, Note: sequence extracted from NCBI C; Keywords: transmembrane protein	A; NCSSITURES: 1 22. CMT.) A; CROSSITURES: 1 25. CMT.) A; Experimental source: C57BL/6 A; Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654) C; Keywords: transmembrane protein

	7;
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	4;
ength 62	Indels 114;
DB 2; I 4e-19;	в 136;
19.8%; Score 336; DB 2; Length 629; 24.7%; Pred. No. 3.4e-19;	1ismatche
; Scor	55; N
19.8%	ative
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ıtch al Sim	100;
Query Match Best Local Similarity 24.7%;	Matches

δ	19	19 AAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTH 78	78
QQ	230	230 AAGKTVVGILGEPVTLPLEFRATRANVWVLNTSVISQERRGAATADSRRKPK 284	284
ò	79	79 RNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT 138	138
qq	285	GSEERRVRISDQDQSLKISQLKMEDAGPYHAYVCSEASRDPSVRHFTLLVYKRLEKPSVT	344
δ	139	139 OSLMASVUSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYT 192	192
Ωp	345	KSPVHMMNGICEVVLTCSVDGGGNNVTYTWMPLQNKAVMSQGKSHLNVSWESGEHLPNFT 4	404
δλ	193	0-	251
qa	405		459
λ̈́O	252	268	268
Db	460	SSLATRYRQAEVPAEIPEPPTGHGQFSVLSQRYE	519

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A, Residues: 1-240 < WON>
A, Cross-references: UNIPROT: P18181; EMBL: X17501; NID: 950134; PIDN: CAA35542.1; PID: 950135. R; Wong, Y. W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
submitted to the EMBL Data Library, June 1990
A, Description: Structure, expression and genetic linkage of the mouse BCMI (OX45 or Blass) a region on mouse chromosome 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sgp-60 as the m
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A;Note: sequence extracted from NCBI backbone (NCBIP:129660)
C;Comment: This antigen is widely expressed on leukocytes and is likely to be anchored t C;Comment: This antigen is widely expressed on leukocytes and is likely to be anchored t C;Superfamily: B-cell surface glycoprotein blast-1
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkac; F;1-22/Domain: signal sequence #status predicted <ATG-P;1-27/Domain: carboxyl-terminal propeptide #status predicted CPT-P;218-240/Domain: carboxyl-terminal propeptide #status predicted covalent) #status predicted F;21,38,70,136,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted P;21/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen BCM1 precursor - mouse
NyAlternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL043; S21319; A47469; B47469
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
A;Exp. Med. 171, 2115-2130, 1990
A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1)
region on mouse chromosome 3.
A;Reference number: JL0143; MJID:90278362; PMID:1693656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  232
                                                                                    121
                                                                                                                                                                         178
                                                                                                                                                                                                                                                                   122 -MEVYDLVSKPAIKIEKTKNLTDSCHLRLSCKV--EDQGVDYTWYEDSGPFPORNPGYVL 178
                                                                                                                                                                                                                                                                                                                                                             179 QIFQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVL 238
GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGD-YKADINTQADPYTTTKRY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 WILLLCLOTWPEAAG-KDSEIFTVNGILGESVTFPVNIQEPRQVKIJAWTSKTSVAYVTP 65
                                                                                                                                                                                                                                                                                                                                                                                                                 :| || :: || || || || || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || 
                                                                                    71 GKK----TVFESVFKDRVDLDKTNGALRIYNVSKEDRGDYÝMRMLHETEDQWKIŤ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A; Mesidues: 1-240 < MONJ.>
A; Residues: 1-240 < MONJ.>
A; Cross-references: EMBL:X53526; NID:950138; PIDN:CAA37604.1; PID:950139
R; Cabrero, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.
R; Cabrero, J.G.; Freeman, G.J.; Jane, 2422, 1993
April: Adentification, by protein sequencing and gene transfection, of
A; Reference number: A47469; MUID:93234508; PMID:8475091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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A;Note: sequence extracted from NCBI backbone (NCBIP:129658)
A;Accession: B47469
                                                                                                                                                                                   125 NLOIYRRLGKPKITOSLMASVNSTCNVTLTCSVEKEEKNVTYNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 179.5; DB 2; 23.6%; Pred. No. 4.3e-07; ative 47; Mismatches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 ILSSVFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: |: |
IIPSILL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 84-98 < CA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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OX-45 membrane glycoprotein precursor - rat
OX-45 membrane glycoprotein precursor - rat
OX-45 membrane glycoprotein precursor - rat
OX-45 membrane mames: MRC OX-45 antigen
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Sep-1899 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C; Accession: S01299
R; Killeen, N.; Mossaner, R.; Arvieux, J.; Willis, A.; Williams, A.F.
EMBO J. 7, 3087-3091, 1988
A; Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the i
A; Reference number: S01299; MUID:89030603; PMID:3181129
A; Accession: S01299
A; Molecule type: mRNA
A; Residues: 1-240 < KLb>
A; Residues: 1-240 < KLb>
C; Superfamily: B-cell surface glycoprotein blast-1
C; Superfamily: B-cell surface glycoprotein blast-1
C; Keywords: glycoprotein; membrane protein; surface antigen
F; 1-22-240/Peroduct: OX-45 membrane glycoprotein #status predicted <AMT>
F; 33-240/Product: OX-45 membrane glycoprotein #status predicted
F; 38, 97, 140, 186, 203/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; nucleic acid sequence not shown
A,Molecule type: mRNA
A,Residues: 1-315 -COC>
A,Cross-references: UNIPROT:Q13291; EMBL:U33017; NID:g984968; PIDN:AAA75380.1; PID:g9849
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                                                                                                                                                                                                                                  J.M.; Yssel, H.; de Vries, J.E.; Aversa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 YLE------NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 YTCTAONPVSNNSDSISARQLCADIAMGFRTH------HTGLLSVLAMFFLLVLILS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 YICTVSNPISNNSQTFSPWPGC-----RTDPSETKPWAVYAGLLGGVIMILIMVVILQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 SVFLFRLFKRR-----QDAASKKTIYTYIMASR-----NTQPAE---SRIYDEILQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LRRRGKTNHYQTTVEKKSLTIYAQVQKPGPLQKKLDSFPAQDPCTTIY--VAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 LLLSLVT----GFQDQSVPNVNAITGSNVTLTILKHPLASYQRLTWLHTTNQKILEYFPN 70
                                                                                              Species: Homo sapiens (man)
.Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGSKVLLPLTYERINKSMNKSIHIVVTWAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                         C;Species: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text
C;Accession: 558992
R;Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.;
Nature 376, 260-263, 1995
A;Title: A novel receptor involved in T-cell activation.
A;Reference number: S58892; MUD:95342241; PMID:7617038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.4%; Score 194; DB 2; Le Best Local Similarity 23.8%; Pred. No. 4.5e-08; Matches 76; Conservative 54; Mismatches 112;
                                                   .gnaling lymphocytic activation molecule - human
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les 62; Conserv
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N;Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 C;Accession: 534338; JC1510; A41093 R;Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G. Bubhitted to the EMBL Data Library, July 1992 A;Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus A;Reference number: S34338
                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g312 R;Across-references: UNIPROT:Q6135; EMBL:X67281; NID:g3128; K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 1993 A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopr. A;Reference number: JC1505; MUID:93273228; PMID:8500759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Generi EggF

Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

C;Superfamily: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F;167-1919/Domain: immunoglobulin homology <IMM1>

F;254-303/Domain: immunoglobulin homology <IMM2>

F;359-396/Domain: immunoglobulin homology <IMM3>

F;319-396/Domain: immunoglobulin homology <IMM3>

F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the carcinoembryonic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biliary glycoprotein A precursor - mouse
N,Alternate names: carcinoembryonic antigen mmCGMla; murine hepatitis virus receptor
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Species: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004
C,Accession: JC1505; A49006; A41563; S11626; S11625
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Status: preliminary
A, Molecule type: protein
A, Residues: 35-59 <WIL>
C, Comment: This protein is expressed at the cell surface and plays a determinant
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 NLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LICDSYTDPDNITYLWSRNGESLSEGDRLKLSEGNRTLTLLNVTRNDTGPYVCETRNPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAQHHL-----WILLL----CLQTW-------PEAAGKDSEIFTVNGILGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LASAHLHKGQVPWVGLLLTASLLASWSPPTTAEVTIEAVPPQVAEDNNVLLLVHNL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 VTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHA----LGPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------PLALGAFAWYKGNPVS----TNAEIVHFVTGTNKTTTGPAHSGRETVYSNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-81, °0', 83-141, 'P', 143-521 < MCC>
A; Croser-references: GB: X67281
A; Croser-references: GB: X67281
B; Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A; Title: Receptor for mouse hepatitis virus is a member (
A; Reference number: A41093; MUID:91288498; PMID:1648219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

8.5%; Score 143.5; DB 2.
Best Local Similarity 23.8%; Pred. No. 0.00099;
Matches 59; Conservative 36; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
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                                                                                                                                                                                                                         A, Accession: S34338
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-521 < HUA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Greezes Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 149443
C; Accession: 149443
C; Matchew, P.A.; Gazni-Wagner, B.A.; Land, K.; Takashima, A.; Stoneman, E.; Bennett, M.; J. Immunol. 151, 528-537, 1993
C; Immunol. 151, 528-537, 1993
C; Matchew, D.A.; Gazni-Wagner, B.A.; Land, K.; Takashima, A.; Stoneman, E.; Bennett, M.; J. Immunol. 151, 528-537, 1993
C; Matchew, D.A.; Gazni-Wagner, B.A.; Land, K.; Takashima, A.; Stoneman, E.; Bennett, M.;
A; Reference number: 149443; MUID:94044757; PMID:822828
A; Accession: 149443
A; Molecule type: mRNA
A; Residues: 1-398 «RES>
A; Cross-references: UNIPROT:Q07763; GB:L19057; NID:g309076; PIDN:AAA16353.1; PID:g309077
C; Genetics:
A; Gene: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 QEL-----TYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPED 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 LILDHVETPNIKAQWKPWTNGTCQLFLSCLVTKDD-NVSYAFWYRGSTLISNQRNSTHWE 184
                                                                                                                                                                                                                |::: : | | | : : : | : | : | | | LEVFDPVPKFSIEINKTEASTDSCHLRLSCEV--KDQHVDYTWYESSGPFPKKSPGYVLD 179
                                                                                                                                                                                                                                                                                                                      VNGILGESVTF-PVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVGVSGKPVQLRPSNIQ-----TKDVSVQW------KKTEQGSHRKIEI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- NTQPAESRIYDEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQ
                                                                         GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTOADPYTTTKRYN
                                                                                                     126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SPLGEEGNVLO
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                WCLVLELLLLPLGTGFQGHSIPDINATTGSNVTLKIHKDPLGPYKRITWLHTKNQKILEY
                                                                                                                                                                                                                                                                                       I FOT PEDQEL TYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.7%; Score 164; DB 2; Length 398; 22.3%; Pred. No. 1.5e-05; Live 49; Mismatches 139; Indels 1
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33; Conservative
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IHRILL 239
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biliary glycoprotein F
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Best Local S
Matches 83
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A; Molecule type: mRNA
A; Residues: 1-521 <MC>
A; Cross-references: UNIPROT: P31809; EMBL:X67279; NID:g50170; PIDN:CAA47696.1; PID:g50171
A; Experimental source: strain CD1; tissue colon
R; Nedellec, P.; Turbide, C.; Beauchemin, N.
Rivedellec, P.; Turbide, T.; Beauchemin, N.
Bur. J. Blochem. 231, 104-114, 1995
A; Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A; Reference number: S65939; MUID:95354678; PMID:7628460
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A,Experimental source: strain BALB/c
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A,Note: only a part of the coding sequence is given
C,Comment: This protein is expressed at the cell surface and plays a determinant role in C,Genetics:
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: |: | | | | | | | | | | BSYTOPDNINYLWSRNGESISEGDRLKLSEGNRTLTLLNVTRNDTGPYVCETRNPVSVNR 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: biliary glycoprotein 1
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JCISO8; S65940; S36852
R;McCualg, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
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A;Molecule type: DNA
A;Residues: 1-21 <NED>
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                                       A Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopromy. Wireference number: 401505, MUID:93273228; PMID:8500759
A; Reference number: 401505
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-458 cMCC>
A; Cross-references: UNIPROT: P31809
B; McCuaig, K.; Turbide, C.; Beauchemin, N.
Cell Growth Differ: 3, 155-174, 1992
A; Title: mmCGMla: a mouse carcinoembryonic antigen gene family member, generated by alter A; Reference number: A49006; MUID:92338096; PMID:1633107
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1-134/Domain: carcinoembryonic antigen precursor amino-terminal homology «CEAN»; 1-34/Domain: signal sequence #status predicted solfs.
15-458/Product: biliary glycoprotein A #status predicted «MHR»; 160-219/Domain: immunoglobulin homology «IMM1»; 254-303/Domain: immunoglobulin homology «IMM1»; 254-303/Domain: immunoglobulin homology «IMM3»; 254-303/Domain: 254-203/Domain: 254-203/Domain: 255-203/Domain: 255-203/Do
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7449-485/Domain: intracellular #status predicted <CYT>
F;71.89;104,148.152,199,206,210,226,588,290,294,304,317,333,375/Binding site: carbohydra
F;167-217,261-301,346-394/Disulfide bonds: #status predicted
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A, Rocession: Sile25
A, Molecule type: manAA
A, Residues: 'PQ', 82-321 < kE2>
A, Cross-references: EMBL:X15351
C; Comment: This protein is expressed at the cell surface and C; Genetics:
A; Gene: BgpA
C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen; Carcinoembryonic antigen; Carcinoembryonic antigen; Carcinoembryonic antigen; Carcinoembryonic antigen; F; 1-34 / Domain: acrinoembryonic antigen precursor amino-term F; 1-34 / Domain: signal sequence #status predicted <SIG>F; 15-454 / Product: biliary Glycoprotein A #status predicted <F; 15-454 / Product: biliary Glycoprotein A #status predicted <F; 15-454 / Product: biliary Glycoprotein A #status predicted <F; 15-454 / Product: immunoglobulin homology <IMM2>
F; 139-36 / Domain: immunoglobulin homology <IMM2>
F; 139-34 / Domain: transmembrane #status predicted <TMN>
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8.4%; Score 142.5; DB 1;
Best Local Similarity 25.3%; Pred. No. 0.001;
Matches 62; Conservative 27; Mismatches 103;
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poliovirus receptor-related protein precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dub Gene 155, 261-265, 1995
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gen A;Reference number: JC4024; MUID:95237621; PMID:7721102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;35-379/Domain: transmembrane #status predicted <TVM>
F;36-379/Domain: transmembrane #status predicted <TVM>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 FDGNWYLQRMDVKLTCKADANPPATEYHWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 YTCTAONPVSNNSDSISARQLCADIAMGFRTH-----HTGLLSVLAMFFLLVLILSSV 243
                                                                                                                                                                                                                                                                                93 NLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVT 152
                                                                                                                                                                                                                                                                                                                                        LICSVEKEEKNVIYNWSPLGE-----EGN-VLQIFQTPEDQELTYTCTAQNPVS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 LTCDSYTDPDNITYLWSRNGESLSEGDRLKLSEGNRTLTLINVTRNDTGPYVCETRNPVS 224
                                                                                                                                                                                                         ------PLALGAFAWYKGNPVS----TNAEIVHQVTGTNKTTTGPAHSGRETVYSNG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKDSEIFTVN----SILGESVTFPVNIQEP-RQVKI--IAWT----SKTSVAYVTP--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----STCNVTLTCSVEKEEKNVTYNWSPLG------EEGNVLQIFQTPEDQEL--T
                                                                                                                                      37 VTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHA----LGPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
                                                           3 LASAHLHKGQVPWVGLLLTASLLASWSPPTTAEVTIEAVPPQVAEDNNVLLLVHNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSETAPVVTVTHRNYYERIHALGPNY---NLVISDLRMEDAGDY--
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A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 INTOADPYTTTKRYNLQIYRRLGKPKITQSLMASVN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 -NNSDSIS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 VNRSDPFS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:PVRR1
                                                                                                                                                                                                                     59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                          Cispecies: Equus cabalius (domestic horse)
Cispecies: Equus cabalius (domestic horse)
Cispecies: Equus cabalius (domestic horse)
Cispecies: Salida (domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycopro
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Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-458 <MCC>
A;Cross-references: UNIPROT:Q61351; GB:X67280
C;Comment: This protein is expressed at the cell surface and plays a determinant role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Asn)
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F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>F;160-219/Domain: immunoglobulin homology <IMM1>F;269-219/Domain: immunoglobulin homology <IMM2>F;389-336/Domain: immunoglobulin homology <IMM3>F;387,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Expression of the Bgp gene and characterization of mouse colon biliary A;Reference number: JC1505; MUID:93273228; PMID:8500759 A;Accession: JC1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSTCNVTLTCSVEKE---EKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSNN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLILSSVFLFRLFKRRQDAASKKTIY 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
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Species: Mus musculus (house mouse)
Jate: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKPP 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell surface glycoprotein CD2 precursor - horse
NiAlternate names: T-lymphocyte surface antigen CD2
C.Species: Equus caballus (demestic horse)
C.Species: 11-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 TILGALERDINLDIPAFOMSEHVEDIQWSKGKTKIAKFKNGS-----MTFQKDKTYEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KNGTLKIKHLERIHEGTYKVDAYDSDGKNVLEETFHLSLLEMVSKPNISW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 TVNGILGESVTFPV-NIQEPRQVKIIAWT-SKTSVAYVTPGDSETAPVVTVTHRNYYERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin,
Gene 127, 173-183, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 49;
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23.8%; Pred. No. 0.0018;
ative 35; Mismatches 95; Indels 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

8.3%; Score 141.5; DB 2; Length 347;
Best Local Similarity 21.2%; Pred. No. 0.00084;
Matches 63; Conservative 49; Mismatches 136; Indels 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 23.8<sup>†</sup>
Matches 59; Conservative
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N.Alternate names: CES; meconium antigen 100
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A53319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098; A26
R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shively, Mol. Cell. Biol. 10, 2738-2748, 1990
A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its pron A;Accession: A36319; MUID:90258861; PMID:2342461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M29540; NID:g180222; PIDN:AAA51967.1; PID:g180223
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and (A;Reference number: A31037; MUID:89122014; PMID:3220478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 PVVTVTHRNYYER-IHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 AQPRKEKETPKEKOTYKLFKNGTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: | | | | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : | : : : | : : : | : : : : | : : : : | : : : | : : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LOTWPEAAGKDSEIFTVNGILGESVTFPV-NIQEPRQVKIIAWTSKTSVAYVTPGDSETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLGKPKITQSLMASVNSTC-NVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #status predicted
                                                                                                                                                                                                                                                                                                                                                      F.25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT> F.25-351/Product: T-cell surface glycoprotein CD2 #status predicted <EXT> F.25-206/Domain: extracellular #status predicted <EXT> F.210-234/Domain: transmembrane #status predicted <TWM> F.237-351/Domain: intracellular #status predicted <INT> F.89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.1%; Score 137; DB 1; Length 351; Best Local Similarity 22.6%; Pred. No. 0.002; Matches 73; Conservative 46; Mismatches 120; Indels
A,Gene: GDB:CD2
A,Cross-references: GDB:118735; OMIM:186990
A,Map position: 1p13.1-1p13.1
A,Introns: 21/1; 128/1; 205/1; 246/1
C,Superfamily: T-cell surface glycoprotein CD2
C,Keywords: glycoprotein; T-cell; transmembrane protein C,Keywords: glycoprotein; T-cell; transmembrane protein F;1-24/Domain: signal sequence #status predicted cSIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVYSEVQFADKMGKASTQDSKPP 319
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A; Residues: 1-702 < BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
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A, Residues: 333-351 <SE3>
R, Seed, B., Azutfo, A.
R, Residues: 333-351 <SE3>
R, Seed, B., Azutfo, A.
R, Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; R, Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; R, Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.
R, Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.
R, Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.
R, Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; A, Accession: S02292
A, Accession: S02292
A, Residues: 1-338, W., 340, 'QokTHCPLPLIKKDRNCLFQ' sAl>
A, Rosidues: 1-338, W., 340, 'QokTHCPLPLIKKDRNCLFQ' sAl>
A, Rosidues: 1-338, W., 340, 'QokTHCPLPLIKKDRNCLFQ' sal>
A, Rolecule type: protein
A, Rolecule type: protein
A, Residues: 25-43, 152-163, sal2
B, Residues: 25-43, 152-163, sal2
B, R, Residues: 25-43, 152-163, sal2
B, R, Residues: 25-43, 152-162, 1988
A, Residues: 25-43, 152-162, 1988
A, Resence number: S00829; MUD: 89005055; PMID: 2901953
A, Andersides: Days
B, A, Accession: Days
B, A, A, A, A, A, A, A, A, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell surface glycoprotein CD2 precursor - human
NiAlternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A;Reference number: A28967; MUID:88144486; PMID:2894031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-351 <DIA>
A,Cross_references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A
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T is closely associated with, the erythrocyte receptor.
Genetics:
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Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A;Title: Molecular cloning of the human T-13mphocyte surface CD2 (T11) antigen.
A;Reference number: A26486; MUID:87041523; PMID:3490670
                                                                                                                   297
315 YICEATNPIGTRSGQVEVNITEFPYTPSPPEHGRRAGPVPTAIIGGVAGSILLVLIVVGG 374
                                                                                                   244 FLFRLFKRRQ----DAASKKTIY--TYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNT
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A;Residues: 25-46,'X',50 <SE2>
K;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A;Reference number: A28416
A;Contents: revision
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A;Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SE1>
A;Accession: B26486
                                                                                                                                                                                                                                                                                                           298 VYSEVQFADKMGKASTQDSK---PPGTSSYE 325
                                                                                                                                                                                                                                                                                                                                                                                                          MAQNLQYPD----DSDDEKKAGPLGGSSYE 438
                                                                                                                                                             : | : | : | | : | 375 IVVALRRRRHTFKGDYSTKKHVYGNGYSKAG----
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A; Molecule type: DNA
A; Residues: 1-351 < LAN>
A; Cross-references: EMBL: X07871
C; Comment: CD2 is a surface
or is closely according
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: A26486
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A;Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat:
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-678/Product: carcinoembryonic antigen #status predicted <MAT>
F;55-2-701/Domain: immunoglobulin homology <IMMI>
F;318-395/Domain: immunoglobulin homology <IMM3>
F;318-315/Domain: immunoglobulin homology <IMM3>
F;608-657/Domain: immunoglobulin homology <IMM4>
F;608-657/Domain: carboxyl-terminal propeptide #status predicted <CTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;679-702/Domain: carboxyl-terminal propeptide form
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R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Tak
RBMO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secrete.
A;Reference number: S12048; MUID:91006015; PMID:2170108
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A; Residues: 1-417 < KOI>
A; Residues: 1-417 < KOI>
A; Crose-references: UNIPROT: P15151; UNIPROT: Q96BJ1; EMBL: X64116; NID: g35809; PIDN: CAA45
A; Crose-references: UNIPROT: P15151; UNIPROT: Q96BJ1; EMBL: X64116; NID: g35809; PIDN: CAA45
A; Note: 67-Ala was also found
A; Note: 67-Ala was also found
A; Note: 61-A; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A; Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and
A; Reference number: A90910; MUID: 89168426; PMID: 2538245
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A; Residues: 1-66,'A', 68-417 <MEN>
A; Cress-references: GB:M29535
C; Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VTHRNYYERIHALGPNYNLVISDLRMEDAGDY-----KAD-INTQADPYTTTKRYNLQIY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 PELPKPSISSNNSKFVEDKDAVAFTC--EPETQDATYLWWVNNQSLPVSPRLQLSNGNRT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 RRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SP---LGEEGNV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Map position: 1943.2-1943.2.
A; Introns: 27/1; 143/1; 244/1; 281/2; 331/1; 384/1; 394/3
C; Superfamily: poliovirus rations: 1991.2.200.000
C; Reywords: alternative splicing; duplication; glycoprotein; receptor; trans F; 1-20/Domain: signal sequence #status predicted <51G>F; 1-41/Product: poliovirus receptor alpha #status predicted <PVRA>F; 21-339,30main: extracellular #status predicted <EXT>F; 21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>
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C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 PVNIQEPRQVKII------AW-----TSKTSVAYV-----TPGDSETAPVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 -----YSGREIIYPNASLLIQNIIQNDTGFYTLHVIKSDLVNEEATG------QFRVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 PFNVAEGKEVLLLVHNLPQHLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 2; Length 702;
.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poliovirus receptor splice form alpha precursor - human
N,Alternate names: poliovirus receptor H20A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 LOIFOTPEDGELTYTCTAQNPVS-NNSDSI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 LTLFNVTRNDTASYKCETQNPVSARRSDSV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 135.5;
24.3%; Pred. No. 0.0
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A, Gene: GDB: PVR; PVS
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;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105; Reference number: A26831; MUID:87326349; PMID:3632664
            A,Cross-references: GB:M29540; NID:g180222; PIDN:AAAS1967.1; PID:g180223
A,Note: the authors translated the codon GTG for residue 130 as Leu
R;Oikawa, S.; Nakazato, H.; Kosaki, G.
Biochem. Biophys. Res. Commun. 142, 511-518, 1987
A;Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA seq
A,Reference number: A25845; MUID:87128144; PMID:3814146
A;Nolecule type: mRNA
A,Nolecule type: mRNA
A,Residues: 5-702 cOIK>
A;Residues: 5-702 cOIK>
A;Cross-references: GB:M15042; NID:g180198; PIDN:AAA51963.1; PID:g180199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S08106
A;Molecule type: mRNA
A;Residues: 5-319,321-702 <012>
A;Coss=references: EMBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638
A;Cross=references: EMBL Data Library, September 1991
B;Barnett, T the EMBL Data Library, September 1991
A;Description: Genomic DNA sequence upstream of the translational start of the carcinoem A;Accession: S31737
A;Reference number: S31737
A;Status: preliminary
A;Molecule type: DNA
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A; Cross-references: GB: M60964; NID:g180215; PIDN:AAA51964.1; PID:g180217
B; Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A; Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon A; Reference number: I59098; MUID:87204247; PMID:3033671
A; Accession: I59098
A; Status: translated from GB/EMBL/DDBJ
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A, Residues: 'X', 140-151,'X', 153,'X', 155-156 < THO>
A, Residues: 'X', 140-151,'X', 153,'X', 155-156 < THO>
A, Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer C, Comment: This heavily glycosylated membane protein of unknown function is a widely use C, Comment: This protein may be processed at its C-terminus. It is anchored to the membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X62151
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembr
A;Reference number: A44476; MUID:93052339; PMID:1427854
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Residues: 331-702 <RE2>
Cross-references: GB:M16234; NID:g180240; PIDN:AAA51972.1; PID:g180241
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B;Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A;Title: Characterization of the genomic organization of human c
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submitted to the EMBL Data Library, September 1989
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A,Map position: 19q13.2-19q13.2
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A;Molecule type: DNA
A;Residues: 1-37 <RES>
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A,Cross-references: EMBI
R,Khan, W.N.; Fraengsmyx
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A;Cross-references: GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
R;Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and indlA;Reference number: A27709; MUID:88268882; PMID:3390172
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A, Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-235;
R; Hefta, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A; Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci)
A; Reference number: A36271; MUID:90256782; PMID:2341397
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R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation A;Reference number: A26414; MUID:87147209; PMID:3469650
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A; Molecule type: protein
A; Mesidues: 35-69 x PAX.
R; Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A; Title: Identification of three new genes and estimation of the size of the carcinoembi
A; Reference number: A44476; MUID:93052339; PMID:1427854
A; Accession: E44476
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F.3-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F.35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F.351-34/Domain: immunoglobulin homology <IWM1>
F.321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F.301-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F.304-111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalent F:309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form
                                                                                                                                                                                                                             CDNAs coding for NCA and
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                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-137, 'L', 139-344 «BAR»
A; Notes references: GBNM29541; NID: 9189103; PIDN: AA59915.1; PID: 9189104
A; Note: the authors translated the codon TTG for residue 138 as Phe
R; Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A; Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen
A; Reference number: A29918; MUID:88139389; PMID:2830274
                                                                                      NID:g189084; PIDN:AAA59907.1; PID:g189085 thdurft. M.A.: Elting, J.J.
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         A;Residues: 11238, VV, 240-344 <TAW>
A;Residues: 1238, VV, 240-344 <TAW>
A;Cross.references: GB:M18728; NID:9189084; PIDN:AAAS9907.1; E
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: B31037
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A;Map position: 19q13.2-19q13.2
A;Introns: 22/1
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A; Residues: 35-141 < KHA>
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A; Residues: 1-344 <NEU>
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A27661

nonspecific cross-reacting antigen precursor - human
NyAlternate names: NCA; TEX/NCA
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1889 #sequence revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R;Olkawa, S.; Kossaki, G.; Makazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A;Title: wholecular cloning of agene for a member of carcinoembryonic antigen (CEA) gene
A;Reference number: A26902; MUID:87298464; PMID:3619891
A;Rocession: A26902
A;Rocession: A29975
A;Molecular cloning of agene belonging to the carcinoembryonic antigen gene fami
A;Reference number: A29875; MUID:87204248; PMID:3033672
A;Rocession: A29975
A;Molecule Lype: DNA
A;Rocession: A29975
A;Molecule Cype: A20975

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 TWHSDLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESFEKPQLLTVN 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 H------GESGSMAVFHQTQGPSYSESKRLEFVAARLGAELRNASLRMFGLRVEDEGN
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                                                                                                                                                                                                                                                                                                                                                                                                                    171;
F;159-223/Domain: immunoglobulin homology <INM1>
F;259-314/Domain: immunoglobulin homology <INM3>
F;344-367/Domain: transmembrane #status predicted <INM3>
F;368-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
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Query Match 7.8%; Score 131.5; DB 2; Length 344;
Best Local Similarity 25.1%; Pred. No. 0.0054;
Matches 54; Conservative 29; Mismatches 67; Indels 65; Gaps
                                                                                                                                                                                                                                                                                 178 LQIFQTPEDQELTYTCTAQNPVS-NNSDSISARQL 211
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compug
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SLF6_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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O91XA0 SLF6_MOUSE	Q8ND32 C244 HUMAN Q9UF04	Q9EQK9 SLAM HUMAN	<u>0960R3</u> 08N713	Q67IP8 Q6UWG1	Q6ZWL4 Q9ESE5	Q6ZR17
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294 351	228 370 42	394 335	335 416	416 198	367	211
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015430; QBWLP1;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Leukccyte antigen CD84 (Leukccyte differentiation antigen CD84 isoform
CD84c) (MAX.3 cell surface antigen precursor) (CD84 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021:3460729; Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.; "Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity with
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Klausherg R.L., Zeberger B., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.P., Zeberge B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hateh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86188202; PubMed=3008886; Andreesen R., Bross K.J., Osterholz J., Emmrich F.; Horresen R., Bross K.J., Osterholz J., Emmrich F.; Human macrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation antigens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97454416; PubMed-9310491; de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.; "CD84 leukocyte antigen is a new member of the Ig superfamily."; Blood 90:2398-2405(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Lymph;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                   328 AA
ALIGNMENTS
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334.5 330.5 323.5 321.5 316.5 315.5

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SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEESVNTVYS 300
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                                                                                                                                                                                                                                                                                                                                                                          1 MAQHHLMILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLITCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS
                                                                                                                                                                                                                                                                                                                                           1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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18082 MW; E78D6D5CAC8D3604 CRC64;
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Catarrhini, Hominidae, Homo.
        Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J.; Submitted (UNI-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR541847; CAG46645.1; -..
InterPro; IPR003189; Ig.
InterPro; IPR003199; Ig.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
NAN TEP PROSITE; PS0835; IG LIKE; 1.
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98.6%; Score 1672.5; DB 2; Length:
Best Local Similarity 96.5%; Pred. No. 2e-123;
Matches 327; Conservative 0; Mismatches 1; Indels
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y12632; CAA73181.1; -.
SWART; SM00409; IG; 1.
                                                                                                                                                                                                                   328 AA; 36861 MW; 6C9A8BDD45BD0344 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 precursor.
                                                                                                                                                                                                                                                       Score 1687; DB 2;
Pred. No. 1.4e-124;
0; Mismatches 1;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.7%;
Matches 327; Conservative 0
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22
339 AA;
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Q8WWI8;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVFLFRLFKRRQDAASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEEPVNTVYS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120
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Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQTPEDQELTYTCTAQNPVSNNSDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVLIL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.9%; Score 1695; DB 2; Length 328; Best Local Similarity 100.0%; Pred. No. 3.2e-125; Matches 328; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAX.3 cell surface antigen.; 6C9A89206A6D0344 CRC64;
                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U82988; AAB84364.1; -.
                                                                                                                                                                                                                                                                                                     EMBL; ACC4015; ARC21721.1; --
EMBL; AJ223324; CAA11264.1; --
EMBL; AJ223324; CAA1264.1; --
EMBL; BC020063; AA420063.1; --
GO; GO: 000592; C: integral to plasma membrane; TAS.
GO; GO: 000592; P: clefense response; TAS.
GO; GO: 0007156; P: homophilic cell adhesion; TAS.
InterPro; IPR001309; Ig.
InterPro; IPR00110; Ig-like.
SMART; SM00409; IG, II-
PROSITE; PS50835; IG_LIKE; 1.
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Last annotation update)
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22 328 M
328 AA; 36871 MW;
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Name=CD84;
Homo sapiens (Human).
                                                                                                                                                                                                         SEQUENCE FROM N.A.
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61 AYVIPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
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Palou E., Freed J.H., Sole J., Pi A., Vilella A., Vives J., Gaya A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U96627; AAD04232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                           Euteleostomi;
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S
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QSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIVI 345
                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.1%; Score 1324.5; DB 2; Length
Best Local Similarity 95.9%; Pred. No. 3.8e-96;
Matches 256; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                           Palou E., Sole J., Pirotto F., Gaya A.;
Palou E., Sole J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF054817, AAF21723.1;
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
SMART; SM00409; IG; I.
PROSITE; PS05155; IG LIKE; I.
SEQUENCE 272 AA; 30514 MW; 6A2E13AA4E22E13E CRC64;
                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD846.
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Last sequence update)
Last annotation update)
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                                                                                       PRT;
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InterPro; IRR00710; Ig-like.
SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                            Name=CD84;
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                                            61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                                                                                                                              SSVFLFRLFKRRQD------AASKKTIYTYIMASRNTQPAESRIYDEILQSKVLP
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                                                                                                          TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, ARFOS481, AAR21722.1; -.
Genew; HGNC:1704; CD84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; 1.
PROSTTE; PSC0835; IG LIKE; 1.
SEQUENCE 345 AA; 38782 MW; DA06BC5A682E62DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
Leukocyre differentiation antigen CD84 isoform CD84a.
Name=CD84;
                                                                                                                                                                                                                                                                                                SKEEPVNTVYSEVQFADKAGKASTQDSKPPGTSSYEIVI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.4%; Score 1669.5; DB 2 94.8%; Pred. No. 3.4e-123; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                       345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.8
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                   1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
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                                                                                  1 MAQHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSV
                                                                                                                                          61 AYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTT
                                                                                                                                                                                                   TKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQI
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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66.3%; Score 1125; DB 2; Length 241;
Best Local Similarity 94.3%; Pred. No. 1.7e-80;
Matches 215; Conservative 2; Mismatches 5; Indels
                            Length 280;
                                                      Indels
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Palou B., Sole J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF054018; AAF21724.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; 1.
SRORTT; SM00409; IG; 1.
SEQUENCE 241 AA; Z6902 MW; F0121BC1609B6C52 CRC64;
31651 MW; A043E048E762A718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
101-07-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD848.
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                           77.8%; Score 1320; DB 2; 100.0%; Pred. No. 8.9e-96;
                                    100.0%; Prec.
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                                                                                                                                                                                                                                                                                                                    SSVFLFRLFKRRQ 253
                                                      Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
280 AA;
                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=CD84;
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SEQUENCE
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THRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPK 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 PEAAGKDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTV
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MEDLINE=20208572; PubMed=10746783;
Palou E., Pirotto F., Sole J., Freed J.H., Peral B., Vilardell C., Vilella R., Vives J., Gaya A.;
"Genomic characterization of CD84 reveals the existence of five isoforms differing in their cytoplasmic domains.";
Tissue Antigens 55:118-127(2000).
EMBL; AF101031; AAF06840.1; --
EMBL; AF101030, AAF06840.1; JOINED.
                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=99180614; PubMed=10079287; DOI=10.1007/s002510050490;
de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 197;
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Last annotation update)
                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte antigen CD84 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.7%; Score 1029; DB 2;
100.0%; Pred. No. 4.8e-73;
ive 0; Mismatches 0;
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197 AA
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PRT;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; 1.
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Name=Cd84; Synonyms=CD84;
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVFLFRLFKRRQDA-----ASKKTIYTYIMASRNTQPAESRIYDEILQSKVLPSKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
Zhou J., Yu W., Tang H., Mei G., TBang Y.T.M., Bouck J., Gibbs R.A.,
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
Tovar V., de la Puente M.A., Pizcueta P., Bosch J., Engel P.;
"Gene structure of the mouse leukocyte cell surface molecule Ly9.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LY9_HUMAN STANDARD; PRT; 655 AA.
20HBG7; 02HA75; 02HA85; 02HQ24;
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen (Cell-surface molecule Ly-9) (CD229 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96128248; PubMed=8537117;
Sandrin M.S., Henning M.M., Lo M.F., Baker E., Sutherland G.R.,
McKenzie I.F.;
                                                                                                                                                                                               13;
                                                                                                                                                         Length 329;
                                                                                                                                                                                               Indels
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                                                                                                                          43BB1AA5AF1989E0 CRC64;
                                                                                                                                                         55.7%; Score 944.5; DB 2;
larity 57.3%; Pred. No. 4.1e-66;
Conservative 48; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIVI 328
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                                   Immunogenetics 51:788-793(2000).
Immunogenetics 49:249-255(1999).
EMBL; AF043445; AAD02273.1; -.
MGD; MGI:1336885; Cd84.
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Immunogenetics 43:13-19(1996).
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Matches 192; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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Margolin J.F.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May participate in adhesion reactions between T lymphocytes and accessory cells by homophilic interaction.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PPO, OCT. 19; 2.

PROSITE; PS50835; IG_LIKE; 2.
Alternative splicing; Antigen; Cell adhesion; Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.
SIGNAL.

1 47 Potential
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V -> M (in Ref. 4).
9FB0A3056D79F80A CRC64;
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EMBL; L42621; AAA92623.1; --
EMBL; AL121985; CAC00580.1; --
EMBL; AYO07142; AAG02002.1; --
Genew; HGNC: 6730; LY9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                   3 QHHLWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVA
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                                                    Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Mus musculus 16 days neonate thyms CDNA, RIKEN full-length enriched library, clone.Al30013D2 product: CDN4 antigen, full insert sequence (Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone.AS30016Al3 product: CD84 antigen, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                               37;
     Length 655;
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MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
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; Score 382.5; DB 1;
; Pred. No. 1.7e-21;
60; Mismatches 100;
  22.6%;
33.9%;
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SEQUENCE FEROM N.A.

STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
MEDLINE=20630913; PubMed=11076861; DOI=10.1101/gr.152600;
A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Mishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Adachi J., Aizawa W. Atalutra T., Arakwa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiranco K., Hiracka T., Hirozane T., Hayashida K., Hayatsu N., Hiracka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T., A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurtoh H., Kawai J., Misuaka T., Misaraki R., Nomura K., Numazaki R., Ohasu M., Ohasu M., Saito R., Saitoh H., Sakai C., Sakai K., Shiraki T., Sogabe Y., Tagami M., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Lomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Embl., AK037385; BAC29799.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.3%; Score 378.5; DB 2; Length 140; 58.3%; Pred. No. 5.4e-22; ive 19; Mismatches 33; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 AA; 16141 MW; EB437F013EF3869D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Aorta and vein, and Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SEQUENCE 140 AA; 16
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Name=Slamf9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (Mouse)
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Les 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1336885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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01-MAR-2002
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Matches
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Query Match
Best Local
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Q8BTK0
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
BA Distchench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
BA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA BAR S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muxny D.M., Sodergren B.J., Lu X., Galbbs R.A.,
Rahesley R., Touchman A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butrerfield Y.S.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RD Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 TSWRPGDKAPSYTCRVSNPVSNISSRRISVGSPCAD--PGYPEKPSMLCLLVKSLFLLLL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SPLGEEGNVLQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.2%; Score 376; DB 2; Length 285; 34.3%; Pred. No. 2e-21; ive 45; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 LAILTVGLCLFRAQKSYETPRVRKLKRNRIKLRKKGKPGPTPV 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LILSSV--FLFRLFKRRODAASKKTIYTYIMASRNTOPAESRI 278
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Zhang W., Wan T., Li N., He L., Yuan Z., Yu M., Cao X.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019477; AAH19477.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1923692; Slamf9.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
SMART: SM00409; IG; 1.
PROSITE; PSO835; IG LIKE; 1.
SEQUENCE 285 AA; 31728 MW; D84BFF8142367F81 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
02-DEC-2004 (TrEMBLrel. 28, Last annotation update)
CD64-H1 (CD2 family 10) (SLAM family member 9).
Name=SLAMF9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor;
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Matches 97; Conservative
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Q96A28;
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Q96A28
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TISSUEPCOLED TERON N.A.

TISSUE-POOLED tissue;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B.L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B.L., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Boat S.E., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 VAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 WILLLCL-----QTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTS
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=21541411; PubMed=11685473; DOI=10.1007/8002510100364;
Fennelly J.A., Tiwari B., Davis S.J., Evans E.J.;
"CD2F-10; a new member of the CD2 subset of the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.0%; Score 373; DB 2; Length 289; 32.1%; Pred. No. 3.6e-21; ive 54; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 LAMFFLLVLILSSVFLFRLFKRRODAASKKTIYTYIMASRNTOPAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32436 MW; 2FB67EE8E4D18205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                      mmunogenetics 53:599-602(2001).
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EMBL; AV034613; AAK61389.1; --
EMBL; BC074754; AAH74754.1; --
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InterPro; IPR007110; Ig-like.
SMART; SM00409; IG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNA sequences.";
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92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Director MGC Project;
Submitted (JUN-2004)
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C TISSUE=B lymphocyte;
A Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Gachi J., Alzawa K., Akimura T., Hara A., Hashizume W.,
Fukuda S., Furuno M., Haramoto K., Hiraoka T., Hirozane T.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Okamura M.,
A Nishi K., Nomura K., Numzazi R., Ohno M., Ohsaron N., Okazaki Y.,
A Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasexi D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A. Takhabahi F., Takaku-Akalira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIŜSUE=B lymphocyte;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus B lymphocyte B cells CRL-1702 WEH 231 cDNA, RIKEN full-
length enriched library, clone:G430073H03 product:weakly similar to
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=B lymphocyte;
MEDLINE=99279223; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Niahi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshika M., Voneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Riken integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Genome Res. 10:1757-1771(2000)
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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     285
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  PRELIMINARY;
                                                                                                                                                                                CD84-H1 (CD2 FAMILY 10)
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TISSUE=B lymphocyte;
The FANTOM Consortium,
                                                                                                                                                                                                                                   musculus (Mouse)
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SPLGEEGNVLQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 IFQTPEDQELTYTCTAQNPVSN-NSDSISARQLCADIAMGFRTHHTGL-LSVLAMFFLLV 237
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM D.A.
The FANTOM COMSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                            6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP
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                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue CDNA, RIKEN full-length enriched
library, clone:2310026104 product:weakly similar to CD84-H1 (CD)
                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                   Score 368; DB 2; Length 28
Pred. No. 8.7e-21;
9; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                48675E0611027B3B CRC64;
MGD; MGI:1923692; Slamf9.

GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR003199; Ig.
InterPro; IPR007110; Ig-like.
SWART; SMO0409; IG; 1.
BROSTIE: PSSO835; IG LIKE; 1.
SEQUENCE 285 AA; 31759 MW; 48675E0611027
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36.5%; Pre-
tive 39;
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SEQUENCE KNOW N.A.

SEQUENCE KNOWN N.A.

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.,

Arakawa T., Bono H., Carninci P., Fukuda S., Pukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Fato H.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konon H., Kowda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Tejima Y., Toya T., Yaammura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,

A Tejima Y., Toya T., Yaammura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO09505; BAB26328.1; -.

R GO; GO:0016021; C:integral to membrane; TAS.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.
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STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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35.2%; Pred. No. 1e-20;
ive 42; Mismatches 117; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUB=Tongue;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sunibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sunibata Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoco R., Matsumoto H., Sakaguchi S., Ikegami T., Rabliwagi K., Pujiwake S., Inoue K., Togawa M., Ohara B., Matahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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SEQUENCE 285 AA; 31764 MW; 33BDB4A633A5C1B3 CRC64;
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LAILTVGLCLFRAQKSYETPRVRK 266
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Matches 93, Conservative
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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AF073415 Mus muscu
AF101030 Homo sapi
AC102471 Homo sapi
AC10241 Homo sapi
AC10241 Homo sapi
AC107193 Sequence
AC90143 Homo sapi
AC1091793 Sequence
L2621 Homo sapi
AX17793 Sequence
BC019477 Mus muscu
AX57541 Sequence
BC019477 Mus muscu
AX377541 Sequence
BC04754 Homo sapi
AX474314 Sequence
BC04754 Homo sapi
AX474314 Sequence
AX77525 Homo sapi
AX474319 Sequence
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AX38159 Homo sapi
AX38159 Homo sapi
AX38159 Homo sapi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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AX474332 Sequence
AX474333 Sequence
AX474241 Sequence
AX924719 Sequence
BC020063 Homo sapi
CQ718714 Sequence
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1. 1040
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, C.C. Cd2001 molecules and uses Cd2000 and cd2001 molecules EP 123218-A 29 17-JUL-2002; Millennium Pharmaceuticals, Inc. (US)
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HSLDACD84
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AF054817
HSU96627
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HSLDA1
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AX474314
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AX034613
AX357479
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AX3574348
AX574548
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AL35596
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    Score:
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U82988 Human leuko
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BD191209 186 human
                                                                                           February 5, 2005, 03:24:06; Search time 5771.83 Seconds (without alignments) 2761.994 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                     nucleic search, using frame_plus_p2n model
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SYT AQH WAX YATT FILL EEP	Oy 182-171-483 (1-329) X NO 3482 (1-1207) Oy 1 MetalaGlaHisHisLeuTrp11eLeuLeuLeuCysLeuGlaThrTrpproGlualahla 20	6 6 6 7	Oy 161 GluLysAsnValThrTyrAsnTrpSerProLeuGluGluGluGluAsnValLeuGlnIle 180
101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsmThrGlnAlaAspProTyrThrThr 120	642 AACAATTCTGACTCCATCTTGCCGGCAGCTCTGTGCAATGGGCTTCCGT 701 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMet PhePheLeuLeuValLeuIleLeu 240 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMet PhePheLeuLeuValLeuIleLeu 240 232 ACCACCACCGGGTTGCTGAGCGTGCTGGCTAGTTCTTCTTCTTCTTTCT	301 GluValGinPheAlaAspLysMetGivLysAlaSerThrGinAspSerLysProProGly 301 GluValGinPheAlaAspLysMetGivLysAlaSerThrGinAspSerLysProProGly 302 GAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGG 321 ThrSerSerTyrGluIlevalIIe 328 323 ThrSerSerTyrGluIlevalIIe 328 324 ThrSerSerTyrGluIlevalIIe 328 325 ThrSerSerTyrGluIlevalIIe 328 326 ThrSerSerTyrGluIlevalIIe 328 327 ThrSerSerTyrGluIlevalIIe 328 328 ThrSerSerTyrGluIlevalIIe 328 329 ThrSerSerTyrGluIlevalIIe 328 320 ThrSerSerTyrGluIlevalIIe 328 320 ThrSerSerTyrGluIlevalIIe 328 321 ThrSerSerTyrGluIlevalIIe 328 321 ThrSerSerTyrGluIlevalIIe 328 322 ThrSerSerTyrGluIlevalIIe 328 323 ThrSerSerTyrGluIlevalIIe 328 324 ThrSerSerTyrGluIlevalIIe 328 325 ThrSerSerTyrGluIlevalIIe 328 326 ThrSerSerTyrGluIlevalIIe 328 327 ThrSerSerTyrGluIlevalIIe 328 328 ThrSerSerTyrGluIlevalIIe 328 329 ThrSerSerTyrGluIlevalIIe 328 320 ThrSerTyrGluIlevalIIe 328 320 ThrSerTyrGluIlevalII	Vertebrata; Euteleostomi; i; Hominidae; Homo. A. logia, Hospital Clinic,

Score: 1695.00 Matches: 328 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 1069.94\$ Indels: 0 DB: 6 Gaps: 0 US-09-882-171-483 (1-329) x BD191209 (1-3173)	Qy 1 MetalaginHisHisLeuTrpIleLeuLeuCeuCysLeuGinThrTrpProGlualaala 20	Qy 21 GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40	Qy 41 ValAsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60 	Oy 61 AlaTyrValThrProdlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80	Oy 81 TyrTyrGluarglleHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArg 100 	Qy 101 MetGluaspalaGlyaspTyrLysalaaspIleAsnThrGlnalaaspProTyrThrThr 120	Oy 121 ThrLysargTyrasnLeuGlnIleTyrargArgLeuGlyLysBroLysIleThrGlnSer 140	Qy 141 LeumetalaserValasnSerThrCysasnValThrLeuThrCysSerValGluLysGlu 160	Qy 161 GluLysasnValThrTyrasnTrpSerProLeuGlyGluGluGlyBsnValLeuGlnIle 180	Qy 181 PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer 200	Qy 201 AsnAsnSerIaSSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220	Oy 221 ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu 240	Oy 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysThr 260	261 IleTyrThrTyrileMetAlaSerArgAsnThrGlnProAlaGluSerArg1leTyrAsp 28	Qy 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluBroValAsnThrValTyrSer 300	301 GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProFroGly 320	Db 951 GAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGG 1010 321 ThrSerSerTyrGlulleVallle 328
Qy 241 SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr 260 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 281 GluIleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer 300	Oy 301 GluValGlnPhealaaspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly 320 	Qy 321 ThrSerSerTyrGlu11eVal11e 328 Db 1030 ACTTCAAGCTATGAAATTGTGATC 1053		DEFINITION 186 numen secreted proteins. ACCESSION BD191209 VERSION BD191209.1 GI:33000948 KEYWORDS JP 2002510192-A/173. SOURCE unidentified	NISM unidentified unclassified. UNCE 1 (bases 1 to 3173)	AUINONS RUBELL, S.M., KOSEN, C.A., T. SOPECT, D.N., CAITEI, N.C., CAITEI, N.C., CAITEI, N.C., CAITEI, C.C., CEGENE, J.M., FROMEN, P. YOUNG, P. E., Greene, J.M., Ferrie, A.M., Duan, R., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y.,	TITLE 186 human secreted proteins JOURNAL Patent: JP 2002510192-A 173 02-APR-2002; HUMAN GENOME SCIENCES INC		0/-MAR-1997 US 60/038621,07-MAR-1997 US 60/040161 PR 07-MAR-1997 US 60/040626,07-MAR-1997 US 60/04034 PR 07-MAR-1997 US 60/04036,07-MAR-1997 US 60/040163 PR 11-APR-1997 US 60/043580,11-APR-1997 US 60/043568 PI STEVEN	M KUBEN, CRAIG A KOSEN, CARRIE L FISCHER, DANIEL R SOPPET, PI KENNETH C CRATER, DANIEL P BEDNARIK, GREGORY A ENDRESS, GUO LIANG PI YU, JIAN NI,		PI LAURIE A BREWER, PAUL A MOORE, YANGGU SHI, DAVID W LAFLEUR PI , YI LI, ZHIZHEN ZENG, PI HLA KYAW PC C12N15,112, C12N5/10, C12N1/21, C07K14/47, C07K16/18, C1201/68, PC		FH Key Location/Qualifiers. FBATURES Location/Qualifiers SOURCE 13173 / Organism="unidentified"	/mol_type="genomic DNA" /db_xref="taxon:32644" ORIGIN	Alignment Scores: 2.85e-157 Length: 3173

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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Morkernan, K.J., Mallah, Y.A., Ganaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Walk, N., Sodergren, E.J., Lu, X., Gabbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butkesley, W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse odna sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                      BC020063 3278 bp mRNA linear PRI 29-JUN-2004
Homo sapiens CD84 antigen (leukocyte antigen), mRNA (cDNA clone
MGC:21324 IMAGE:4385965), complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Stransbergy,R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
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1186 human screted proteins
Patent: EP 1352962-A 174 15-OCT-2003;
HUMAN GENOME SCIENCES, INC. (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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/product="CD84 antigen (leukocyte antigen)"
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FRITHTGLLSVLAMFFLLVILILSSVPELFRLFKRRQDAASKKTIYTYINASRNYQPAES
RIYDEILQSKVLPSKEEPVNTVYSEVQFADRMGKASTQDSKPPGTSSYEIVI"
                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 26 Row: o. Column: 19
This clone was selected foor full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502686. Location/Qualifiers

1. 3278
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Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                                                                                                                                                                                                                                                                 Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                       Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
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/gene="CD84"
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/ voidence=experimental
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/ db xref="G0A:015430"
/ db xref="G0A:015430"
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                                                                                                                              07-APR-2000
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                                                                                                                                                                                                                                                                                                                      cell surface antigen; glycoprotein; MAX.3 antigen.
Homo sapiens (human)
Homo sapiens
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Krause, S.W.
Direct Submission
Submitted (05-FEB-1998) Krause S.W., Hematology, University of
Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042,
GERWANY
          GlulleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer
                                                                                                                GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly
IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp
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/product="MAX.3 cell surface antigen"
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/orge="many"
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328
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Matches:
Conservative:
Mismatches:
Indels:
                  thereof
Patent: WO 02068579-A 4648 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. 3296
/ Organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                   (1-3296)
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This clone is available from RZPD, Contact RZPD (customer.service@rzpd.de) for further information. Contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD. This CDS has been cloned without stopcodon. This CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. AAAAAA GGA GGC TCC ACC (ATG). The last codon is followed by the 3' att site: GACCCAGCTTCTT. att The last codon is validated by full sequence check. Compared to the reference sequence NM_003874 (GI:4502686) we found AA exchange(s) at position (first base of changed triplet):
CR541847 1nnear PRI 29-JUN-2004
Homo sapiens full open reading frame CDNA clone RZPDo834H0132D for
gene CD84, CD84 antigen (leukocyte antigen); complete cds, without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germany
FZPD; RZPD0834H0132D, ORFNo 3790
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0132D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 994)
Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Cloning of human full open reading frames in Gateway (TM) system entry vector (poonR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total to 984)
Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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/db_xref="taxon:9606"
/clone="RZPDo834H0132D"
/clone lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
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Location/Qualifiers
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                                                                                                 1005 ACTTCAAGCTATGAAATTGTGATC 1028
                                                                   321 ThrSerSerTyrGluIleValIle 328
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Full ORF shuttle clone,
Homo sapiens (human)
Homo sapiens
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/gene="CD84"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       645 AACAATTCTGACTCCATCTCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGT
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DB:
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No.:
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/organism="Homo sapiens"
// program: "Homo sapiens"
// db _xref="taxon:9606"
// db _xref="leukpcyte"
// clone lib="lambda gt10"
// o. .1089
// o. .1080
// o. .1089
// o. .1089
// o. .1080
// o. .108
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                            GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly
                                                                                                                                                                                                                              GlulleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer
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H.sapiens mRNA for leukocyte differentiation antigen CD84.
Y12632
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/product="leukocyte differentiation antigen CD84'
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leukocyte differentiation antigen.
Homo sapiens (human)
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      1. .>984
// gene="CD84"
// codon_start=1
// codon_start=1
// protein_id="CAG46645.1"
// db_xref="G1:49456649"
// codon_start=1
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DAGDYKADINTQADPYTTTRRYNLQYTRAGAFTTTOSLAGANSCTONTLTCSVEKE
BKNYTYNWSPLGEEGNVLLICSSVEFERDEDGETTTCTAQNPVSNNSDSISARQLCADIANG
FRTHHTGLLSVLAMPFELLVLILSSVEFERDENGERSVENGSASKKTIYTYTNASRAYQPAES
RIYDEILQSKVLPSKEESVNTVYSEVQFADKMGKASTQDASKKTIYTYTNASRAYQPAES
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q ò В Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1118)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers

GI:6650107

AF054816.1

Homo sapiens (human)

sapiens

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70. .1107

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ORGANISM
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AUTHORS
TITLE
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KEYWORDS
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AF054816 1118 bp mRNA linear PRI 01-JAN-2000 Homo sapiens leukocyte differentiation antigen CD84 isoform CD84a (CD84) mRNA, complete cds. AF054816

DEFINITION

ACCESSION

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SM Homo sapiens

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Matazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 967)

RS Palou, E., Sole, J., Pirotto, F. and Gaya, A.

Direct Submission

AL Submission

Direct Submission

Nilarroel 170, Barcelona 08036, Spain

SS Location/Qualifiers

Jordanism="Homo sapiens"

Mollarroel 170, Barcelona 08036, Spain

Jordanism="Homo sapiens"

Jordanism="Homo sapiens
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                                                                                                                      AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg
                                                                                                                                                                                                                          ThrHisHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu
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240 220 789 260 100 369 120 429 ThriyaArgTyrAsnLeuGln1leTyrArgArgLeuGlyLy8ProLy81leThrGlnSer 140 489 160 549 180 609 200 699 729 249 9 ASIABRISERABPSERILESERALAARGUNLEUCYSALAABDILEALAMETGIYPHEARG SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp ThrHisHisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeulleLeu PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer ValasnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal rcricagigiririgirccgrrrgrrcaagagaa------967 294 1 0 34 Length: Matches: Conservative: Mismatches: Indels:

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1 (Bases 1 to 888)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.

Direct Submission
Submitted (20-MRR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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250 GCTTATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCCACAGAAAT
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                                                                                                                                                                                                                                              430 accaagceracaaccrecaaarcrarcercegerreegaaaccaaaarracacagarr
                                                                                                                                                                                                                                                                                                              Homo sapiens leukocyte differentiation antigen CD84 (CD84) mRNA, complete cds.
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Homo sapiens CD84 mRNA, alternatively spliced, complete cds.
U96627.1 GI:4100318
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Palou,E., Freed,J.H., Sole,J., Pi,A., Vilella,A., Vives,J. and
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Submitted (07-APR-1997) Servei Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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55. .1044
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                                     Molecular cloning, characterization, and chromosomal localization of the mouse homologue of CD84, a member of the CD2 family of cell
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Bosch, J. and
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GCTTTTATAAAACCAGGAGTCAATAAAGCTGAA-----GTTACCATAACCCAGGGCACT
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de la Fuente, M.A., Tovar, V., Pizcueta, P. and Engel, P.

de la Fuente, M.A., Tovar, V., Pizcueta, P. and Engel, P.

Direct Submission
Submitted (17-51AN-1998) Immunology Unit, Department of Cellular
Biology, Medical School, University of Barcelona, Casanova 143,
Barcelona 08036, Spain
Location/Qualifiers
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Fuente, M.A., Tovar, V., Pizcueta, P., Nadal, M.,
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Matches:
Conservative:
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Immunogenetics 49 (4), 249-255 (1999)
99180614
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Mus musculus CD84 leukocyte antigen (CD84) mRNA, complete cds.
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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4, 2005, 11:54:40; Search time 89.3239 Seconds (without alignments) 861.643 Million cell updates/sec
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1039
1 KDSEIFTVNGILGESVTFPV.......NNSDSISARQLCADIAMGFR 199
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SUMMARIES

PRO polyp Human sec Human nov Region of Novel hum Human sec Human leu Human sof Human CD8 Human PRO Aab47878 SCZ/CD84 Human Human Human Human Human Human Human Description Adp23943 Aaw74891 Abo345343 Abo345343 Adi21198 Adi7220 Adi5722 Adi6772 Adi6772 Adi67782 Adi67782 Adi67782 Adi67782 Adi67782 Adi67783 Adi67 Ad182907 1 Ad182907 1 Ad005708 1 Adq19067 1 ADL57105 ABG96270 AAU74425 ADL57103 ADO63782 ADO78174 ADI23198 ADH74200 AAE26238 ADL82907 ADO05708 ADQ19067 ADP23943 AAW74891 ABG95343 ADL57243 ADK98560 AAB47878 AB034537 Query Match Length DB Score 10039 . No. Result

Aae12078 Dendritic	m	1 Human	~	Hypoxi	Human	Human	1 Human	Aae26250 Human CD	Human	~	Human	Aae26232 Human CD2	1 Human	Aae26222 Human CD2	1 Human	<u>ო</u>) Human	Abr39107 Human NTB	Abu03145 Human imm	TS			
AAE12078	AAE26243	AAE26251	AAE26253	ABP65110	ABW01823	ABW01833	ABW01831	AAE26250	ABW01830	AAE26252	ABW01832	AAE26232	ABW01811	AAE26222	ABW01801	ABB90183	AAE26220	ABR39107	ABU03145	ALIGNMENTS		328 AA.	
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			SCZ; CD84; platelet; monocyte; circulating B cell; schizophrenia; allele; polymorphic marker; chromosome 1q22.
			; circulatir e 1q22.
AAB47878;	02-MAY-2002 (first entry)	SCZ/CD84.	SCZ; CD84; platelet; monocyte; circu polymorphic marker; chromosome 1q22.
	AAB47878;	AAB47878; 02-MAY-2002 (first entry)	AAB47878; 02-MAY-2002 (first entry) SCZ/CD84.

23-APR-2001; 2001WO-US013040 21-APR-2000; 2000US-0198873P WO200202054-A2. Homo sapiens. 10-JAN-2002

(RUTF) UNIV RUTGERS STATE NEW JERSEY. Brzustowicz LM, Bassett AS;

WPI; 2002-171605/22. N-PSDB; AAI72383.

Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1q22, were the marker is linked to a variant form of the SCZ gene.

Example 6; Page 70; 82pp; English.

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Human Human

6666666£

ABW01826 AAE26249

AAE26246

Human Human

This sequence is encoded by the SCZ gene which was isolated using the method of the invention. The SCZ gene has been previously identified as CD84, GenBank Accession No: NM 003874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. This protein may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method comprises determining the presence or absence of an allele of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1q22 and is linked to a gene (SCZ) having

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like domains and SLAM associated protein, termed CD2000 or CD2001, usefu
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                                                                                                                                                                              22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
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                                                                      Length 328;
a variant form associated with a phenotype of schizophrenia
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ive 0; Mismatches 0;
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and SLAM associated protein (SAP) motifs. CD2000 DNA and protein is useful for treating disorder such as immune proliferative disorders, immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple socierosis, Garve's disease, and Hashimoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (AIDS)), inflammatory disorders (e.g. crohn's disease and ulcerative (c.ditts), inflammatory disorders (e.g. theumatory syndrome octoarthritis), allergic inflammatory disorders (e.g. asthma and cortacthritis), apoptotic disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytocoxic disorders, espetic shock, cronic obstructive pulmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical crials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASVNSTCNVTLTCSVEKEEKNVTYNMSPLGEEGNVLQI PQTPEDQELTYTCTAQNPVSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVHRNY
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 328;
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                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1039; DB 5; 100.0%; Pred. No. 6.7e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dennis K, Fong S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL82907 standard; protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSDSISAROLCADIAMGER 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-2002; 2002US-0411392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO24934, SEQ ID 109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark H,
                                                                                                                                                                                                                                                                                                                                                                   Sequence 328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004024097-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL82907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL82907
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The invention relates to treating a subject having a condition that benefits from modulating the balance of regulatory T cell function to relative to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1, CG PRR-32, CD89, GD89, serctonin R, BY55, serctonin R20, PDB-4d, and PI-CG histamine R-H4, GPR58, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDB-4d, and PI-CG are useful for diagnosing, preventing or treatment occurs. The methods are useful for diagnosing, preventing or treating conditions or regulatory T cell response to antigens associated with the condition, such as in an claim response, an autoimmune disorder, a viral infection, a microbial infection, a parasitic infection a tumour. The present sequence represents a human leukocyte differentiation CD84 antigen, preferentially expressed in regulatory T cells.
                                                                                                                                                                                                                                                                                                    Treating a condition that benefits from modulating regulatory or effector T cell function comprises administering an agent that modulates the expression or activity of a gene or polypeptide (e.g. PTGER2, TGFbetal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1039; DB 8; Length 328; 100.0%; Pred. No. 6.7e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human soft tissue sarcoma-upregulated protein - SEQ ID 1886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Example, SEQ ID NO 8; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ19067 standard; protein; 328
09-0CT-2002; 2002US-0417243P.
18-0CT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424777P.
08-NOV-2002; 2002US-042488IP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Jagged-1 or GPR-32).
                                                                                                                                                                                                              WPI; 2004-340801/31.
N-PSDB; ADO05707.
                                                                                                                                                                    Szymanska G;
                                                                                                                     (TOLE-) TOLERRY INC
                                                                                                                                                                                                                                                                 GENBANK; 6650105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                    Rao P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
ADQ19067
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         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                           The present invention relates to PRO proteins and their coding sequences.
The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide antigen unresponsiveness, selective IgA deficiency, intermediate lymphoma, follinemia of infancy, Burkit's lymphoma, intermediate lymphoma, follicular lymphoma, type II hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 MASVNSTCNVTLICSVEKEERAVIYNWSPLGEEGNVLQIFQTFEDQELTYTCTAQNPVSN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                            New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylltis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; CD83; leukocyte differentiation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1039; DB 8;
Best Local Similarity 100.0%; Pred. No. 6.7e-88;
Matches 199; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte differentiation antigen CD84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD005708 standard; protein; 328 AA
                                                                                                                                                                              Claim 10; Fig 109; 695pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSDSISAROLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 NSDSISARQLCADIAMGFR 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
              WPI; 2004-329389/30
                                       N-PSDB; ADL82906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 328 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2004
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> RESULT 4 AD005708

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarched of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic sarcoma, possibly via gene therapy or vaccine production. The nucleic fact sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLOIFOTPEDOELTYTCTAONPVSN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAONPVSN 180
                                                                                                                                                                                                                                                                                 :ly detection of soft tissue sarcoma comprises determining expression a gene in a first soft tissue sample and a normal soft tissue sample I comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antialergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1039; DB 8; Length 328; larity 100.0%; Pred. No. 6.7e-88; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 1886; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP23943 standard; protein; 328 AA.
                                                                                                                                                                                                   Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSDSISARQLCADIAMGFR 220
                                                                                                                                                         (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO polypeptide SEQ ID NO:1121.
                                                                             26-NOV-2003; 2003WO-US038193.
                                                                                                                     26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                 Early detection of soft
                                                                                                                                                                                                   Ginsburg WM,
                                                                                                                                                                                                                                         WPI; 2004-441208/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 199; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 328 AA;
WO2004048938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                   10-JUN-2004
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The invention relates to a nove isolated increased and the proposition has antinfilammatory, antiatheritic, antirheumatic, immunosuppressive, osteopathic, antidabatic, dermatological, antipportatic, antidalergic, antiasthmatic, hepatotropic, and respiratory activity. A polymuclectide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogram's syndrome, systemic sclerosis, antidopathic inflammatory myopathy, Sjogram's syndrome, trombocytopenia, thyroiditis, diabetes mellitus, immune-mediated area in disease, a demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, Guillainy crimpses, and inflammatory demyelinating polyneuropathy, Guillainy chimary disease, infectious or autoimmune chronic active hepatitis, primary disease, infectious or autoimmune chronic active hepatitis, primary clinflammatory bowel disease, contact dermatitis, solerosing chlamatory bowel disease, contact dermatitis, postiasis, an allergic clisease, asthma, allergic rhinitis, attendiated skin disease, a bullous skin disease, asthma, allergic rhinitis, attendiated skin disease, bullous contact dermatitis, contact dermatitis, food chromonia, idiopathic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity, urricaria, an immunologic disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein or contact disease, graft rejection or cortact dermatical sequence represents a PRO protein
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                                                                                                                                                                                                                                                                                                                                                                                                                            New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
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100.0%; Pred. No. 6.7e-88;
ive 0; Mismatches 0;
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                                                                                                                            30-OCT-2003; 2003WO-US034312.
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                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a secreted human protein encoded by the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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97US-0057669P.
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N-PSDB; AAV59674.
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22-AUG-1997;
22-AUG-1997;
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12-SEP-1997
Human, secreted protein; testis; tumour; foetal brain tissue;
fusion protein; cancer; central nervous system; seizure; diagnosis;
neurodegenerative disease.
                                                                                                                                         Human secreted protein encoded by gene 164 clone HSAWF26.
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                                                         AAW74891 standard; protein; 329 AA.
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/label= unknown
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     acid molecule designated Gene 164 from the human cDNA clone HSAWF26 (deposited as clone ATCC 97903 and ATCC 209049). The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAVS9502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (mucleic acid sequences: AAV59511-V59812; amino acid sequences AAM731-W73026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymucleotides. Specific uses are described for each of the 186 polymucleotides, based on which tissues they are most highly expressed in (see AAVS9511 for
                                                                                                                                                                                                                                                                                                                                                       82 YERIHALGPNYNLVISDLRMEDAGDYRADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral isohaemia; angiogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive;
                                                                                                                                                                                                                                                                         22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAMTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                          61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
                                                                                                                                                                                                                                                           1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                           100.0%; Score 1039; DB 2; Length 329; 100.0%; Pred. No. 6.7e-88; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG95343 standard; protein; 329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel secreted protein #164.
                                                                                                                                                                                                                                                                                                                                                                                                         181 NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                        202 NSDSISARQLCADIAMGFR 220
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97US-0040161P.
97US-0040162P.
97US-0040333P.
97US-0040334P.
97US-0040334P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preservative; nutritional:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2003 (first entry)
                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 199; Conservative
                                                                                                                                                                                      Sequence 329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6420526-B1
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
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07-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG95343;
                                                                                                                                                                                                              Query Match
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperpolificative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, particular disorders e.g. corneal infection. The polypeptides e.g. and coular disorders e.g. corneal infection. The polypeptides can also be used to aid wound the healing and epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotrais. The polypeptides can also be used as a food additive or preservative to carbohydrate, vitamins, minerals, cofactors and other nutritional components. The printed specification, but was obtained in electronic format disparal, from memory at contact.
                                                                                                                                                                                                                                                                                                                                                                                                                 Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;
Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 v isolated human secreted protein for diagnosing, preventing, treating
ameliorating medical conditions and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directly from USPTO at segdata.uspto.gov/sequence.html?DocID=6420526B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1039; DB 5; Length 329; 100.0%; Pred. No. 6.7e-88; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 483; 129pp; English.
97US-0056884P-
97US-0056884P-
97US-0056887P-
97US-0056889P-
97US-0056899P-
97US-0056899P-
97US-0056899P-
97US-0056891P-
97US-0056891P-
97US-005691P-
97US-0056911P-
97US-0056911P-
97US-0056911P-
97US-0056911P-
97US-0056911P-
                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                    98WO-US004493
                                                                                                                                                                                                                                                                                                                97US-0058785P
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Matches 199; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 329 AA;
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                                   22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
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Human; secreted protein; hyperproliferative disorder; leukaemia;
breast cancer; wound; reproductive disorder; blood-related disorder;
haemophilia; thrombocytopeania; immunodeficiency; thymic hypoplasia;
wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;
graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;
wiral infection; bacterial infection; fungal infection; AIDS; sepsis;
we main disorder; kidney failure; cardiovascular disorder; cycostatic;
mangina pectoris; cerebral ischaemia; congenital heart defect;
mangina pectoris; cerebral ischaemia; congenital heart defect;
parkinson's disease; inflammation; Crohn's disease;
manticoagulant; neurological disorder; hlombolytic;
manticoagulant; neuroprotective; thyromimetic; thrombolytic;
antiasthmatic; virucide; fungicide; antiallergic;
matiasthmatic; virucide; fungicide; antialparkinsonian;
             121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN
                                                                                                                                                                                                               Region of human secreted protein encoded by cDNA sequence #164.
                                                                                                                                          ABO34537 standard; protein; 329 AA.
                                                   181 NSDSISARQLCADIAMGFR 199
                                                                         202 NSDSISARQLCADIAMGFR 220
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97US-0040163P.
97US-0040163P.
97US-0040333P.
97US-0040334P.
97US-0040331P.
97US-0043312P.
97US-0043312P.
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97US-0047503P.
97US-0047581P.
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                                                                                                                                                                                            22-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003049618-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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23-MAY-1997;
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ABO34537
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97US-0047582P

YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120 YERIHALGPNYNLVISDLRMEDAGDYRADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141

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23 - MAY - 1997; 97US - 0047583 P.
23 - MAY - 1997; 97US - 0047584 P.
23 - MAY - 1997; 97US - 0047586 P.
23 - MAY - 1997; 97US - 0047586 P.
23 - MAY - 1997; 97US - 004758 P.
23 - MAY - 1997; 97US - 004758 P.
23 - MAY - 1997; 97US - 004758 P.
23 - MAY - 1997; 97US - 004758 P.
23 - MAY - 1997; 97US - 004758 P.
23 - MAY - 1997; 97US - 004758 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004759 P.
23 - MAY - 1997; 97US - 004761 P.
23 - MAY - 1997; 97US - 004761 P.
23 - MAY - 1997; 97US - 004761 P.
23 - MAY - 1997; 97US - 004761 P.
24 - MUC - 1997; 97US - 00568 P.
25 - MUC - 1997; 97US - 00568 P.
25 - AUG - 1997; 97US - 00568 P.
25 - AUG - 1997; 97US - 00568 P.
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25 - AUG - 1997; 97US - 00568 P.
26 - AUG - 1997; 97US - 00568 P.
27 - AUG - 1997; 97US - 00568 P.
28 - AUG - 1997; 97US - 00568 P.
28 - AU
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The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide sequences for the secreted proteins are useful for preventing, treating, andiotaxing or disgoorders less in the secreted proteins are useful for preventing, treating, conclusions and polymorleotide sequences for the secreted proteins are useful for preventing, treating, conclusions in munucledifications, wounds, reproductive disorders, blood-related disorders (e.g. haemophilia or thrombootycopaenia), immunodefactionies (e.g. hashophilia or thrombootycopaenia), immunodefactions (e.g. graft-versus-host disease, thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease, wital or bacterial or thugal infections (e.g. AIDS or sepsia), renal disorders (e.g. kidney failure), cardiovascular disorders (e.g. asthma), infections (e.g. AIDS or sepsia), respiratory disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina pectoris, carebral ischemia or congenital heart defects), respiratory continuodeotide or polypoptide may also be used as vaccine adjuvants. ABO34374-ABO34815 represent human secreted proteins or their fragments. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the cuspic secured proteins or their fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral ischemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Bndress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan DR, Hu J, Florner KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1039; DB 6; Length 329; 100.0%; Pred. No. 6.7e-88; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 483; 260pp; English.
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Matches 199; Conservative
                                                                                                                YU G.
NI J.
FENG P.
COUNG P.
GREENE J M.
FERRIE A M.
DUND R.
FUOLENCE K A.
            RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
                                                                                                                                                                                                                                                                                             FISCAL
EBNER R.
                                                                                                                                                                                                                                                                             OLSEN H S.
FISCHER C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-521800/49.
N-PSDB; ACD82804.
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                                                                                                                                                                                                                                                                                                                            BREWER L A.
MOORE P A.
SHI Y.
                                                                                                                                                                                                                                                                                                                                                                                 (LAYL/) LAFLEUR I
(LIYY/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
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                                                               (CART/)
(BEDN/)
(ENDR/)
(YUGG/)
(NIJJ/)
(FENG/)
                                                                                                                                                                                       (GREE/)
(FERR/)
(DUAN/)
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(FLOR/)
(OLSE/)
(FISC/)
                                                                                                                                                                                                                                                                                                             (EBNE/)
(BREW/)
(MOOR/)
(SHIY/)
                                (ROSE/)
(SOPP/)
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9 81

Gaps

KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAMTSKTSVAYVTPGDSETAPVVTVTHRNY 1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY

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9710S-0047595P.
9710S-0047596P.
9710S-0047599P.
9710S-0047599P.
9710S-0047601P.
9710S-0047613P.
9710S-00476114P.
9710S-0056611P.
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9705-0056909P-
9705-0056910P-
9705-0057650P-
9705-0057669P-
9705-005761P-
9705-005781P-
9705-0057818-
9705-0051860P-
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2000US-0190068P
2001US-00809391
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
YU G.
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17-MAR-2000;
16-MAR-2001;
       23 - MAX - 1997;
23 - MAX - 1997;
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23 - MAX - 1997;
24 - MAX - 1997;
25 - MAX - 1997;
26 - JUN - 1997;
66 - JUN - 1997;
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22-AUG-1997;
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16-JUL-1997;
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09-OCT-1997;
06-MAR-1998;
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997,
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22-AUG-1997
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(ROSE/)
(SOPP/)
(CART/)
(BEDN/)
(ENDR/)
(YUGG/)
YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                     82 YERIHALGPNYNLVISDLRMEDAGDYRADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                           cytostatic; gene therapy; cancer; human; secreted protein
                                                                                                                                                                                                                        Novel human secreted protein seq id 483.
                                                                                                                                                               ADI23198 standard; protein; 329 AA.
                                                                                       NSDSISARQLCADIAMGFR 199
                                                                                                    202 NSDSISARQLCADIAMGFR 220
                                                                                                                                                                                                                                                                                                                                              97US-0038621P.
97US-0040162P.
97US-0040133P.
97US-0040334P.
97US-0040334P.
97US-0040331P.
97US-0043311P.
97US-0043311P.
97US-0043312P.
97US-0043312P.
97US-0043312P.
97US-0043312P.
97US-0043312P.
97US-0043312P.
97US-0043312P.
97US-0043569P.
97US-0043569P.
97US-0043569P.
97US-0043569P.
97US-0043569P.
97US-0047569P.
97US-0047569P.
97US-0047560P.
97US-0047581P.
                                                                                                                                                                                                                                                                                                                            18-JUN-2001; 2001US-00882171
                                                                                                                                                                                                      22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                     US2003175858-A1.
                                                                                                                                                                                                                                                                                                                                                                                     07-WAR-1997;
07-WAR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-MAY-1997;
3-MAY-1997;
3-MAY-1997;
3-MAY-1997;
3-MAY-1997;
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997;
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-MAY-1997;
-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      997;
                                                                                                                                                                                                                                                                                                         18-SEP-2003
                                                                                                                                                                                   ADI23198;
           61
                                                                                         181
                                                                                                                                          RESULT 10
ADI23198
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human; secreted protein; cancer; haematopoietic disorder; endocrine disorder; immune system disease; inflammatory disorder.
                                                                                                                                                                                         970S-0038621P-
970S-0040161P-
970S-0040163P-
970S-0040334P-
970S-0040331P-
970S-00403311P-
970S-0043313P-
970S-0043313P-
970S-0043313P-
970S-0043313P-
970S-0043313P-
970S-0043576P-
970S-0043576P-
970S-0043576P-
970S-0043576P-
970S-004369P-
970S-004369P-
970S-004369P-
970S-0047502P-
970S-0047502P-
970S-0047503P-
970S-0047581P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9705-0047596P-
9705-0047596P-
9705-0047598P-
9705-0047600P-
9705-0047601P-
9705-0047612P-
9705-0047614P-
9705-0047614P-
9705-0047613P-
9705-0047613P-
9705-0047613P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0047618P.
97US-0047632P.
97US-0047633P.
97US-0048964P.
97US-0048974P.
                                                                                                                                                              10-JUN-2002; 2002US-00164861
             Human secreted protein #164
                                                                                                          US2003225248-A1.
                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  11-APR-1997;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                         11-APR-1997;
11-APR-1997;
                                                                                                                                     04-DEC-2003
                                                                                                                                                                                                                                                                                            07-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-MAY-1997
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a polypucleotide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or amelicating as medical condition e.g., cancer. The is the amino acid sequence of a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 YERIHALGPNYNLVISDLRAMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTÞGDSETAPVVTVTHRNY 60
                                                                                                                                                                                                                                         Endress GA, Yu G, Ni J, Feng P, Young PE, Greene UM, Ferrie AM; Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R; Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z. Kvam H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 1039; DB 7; Best Local Similarity 100.0%; Pred. No. 6.7e-88; Matches 199; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID NO 483; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH74200 standard; protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSDSISARQLCADIAMGFR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2004 (first entry)
        YOUNG P E. GREENE J M. FERRIE A M. DUAN D R. HU J. FLORENCE K A.
                                                                                          OLSEN H S.
FISCHER C L.
EBNER R.
BREWER L A.
MOORE P A.
SHI Y.
                                                                                                                                                                                                                                                                                                                     WPI; 2003-898535/82.
                                                                                                                                                                            LAFLEUR D W
                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADI22889
                                                                                                                                                                                                        ZENG Z.
KYAW H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 329 AA;
                                                                                                                                                                                                                                                                                                                                                                                         e.g., cancer.
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                                                                                                                                                                           (LAFL/) | (LIYY/) | (ZENG/) | (KYAW/) |
                                                                                           (OLSE/)
(FISC/)
(EBNE/)
                                                  (DUAN/)
(HUJJ/)
(FLOR/)
          (YOUN/)
                                                                                                                                     BREW/)
                                                                                                                                                    MOOR/
                                     FERR/
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The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPs) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoietic disorders, endocrine disorders, diseases of the immune system, inflammatory disorders and many others. Pull details of disorders that may be prevented, diagnosed and/or treated by the above methods are given in the specification. The nucleic acid molecules may be used to produce their proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The SPs may also be used as antigens in the production of antibodies against the proteins and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Soppet DR, Carter KC, Bedni, Yu G, Ni J, Feng P, Young PE, Grei J, Florence KA, Olsen HS, Fischer CI Moore PA, Shi Y, Lafleur DW, Li Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SEQ ID NO 483; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aberrant expression and activity.
9705-0051926P.
9705-0055214P.
9705-0055631P.
9705-0056631P.
9705-0056631P.
9705-0056631P.
9705-0056631P.
9705-0056631P.
9705-0056631P.
9705-0056631P.
9705-005681P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0057761P
97US-0058785P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00149476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7US-0061060P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-131264/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADH73891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endress GA, Y
Duan R, Hu J,
                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                                                                                                            22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                     .997
                                                                                                                                                 , 766
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22-AUG-1997
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22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                             22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brewer LA,
              16-JUL-1997
                                                                                      997
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                                                                                                                                                                                                                         22-AUG-1997
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22-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                         22-AUG-19
                                    22-AUG-1
22-AUG-1
22-AUG-1
22-AUG-1
22-AUG-1
                                                                                                22-AUG-1
22-AUG-1
                                                                                                                                    22-AUG-1
22-AUG-1
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Ferrie AM; Kyaw H;

Bednarik DP; , Greene JM, Fe cher CL, Ebner R Zeng Z,

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/label= RLRKPKITWSLRHSEDGICRISLTCSVEDGGNTVMYTWTPLQKEAVVSQ
GESHLMVSWRSSENHPNLTCTASNPVSRSSHQFLSENICSG
/note= "Optionally absent"
                                                                                                                                                                                                                                                                                 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
                                                                                                                                                                                                                                                                                                     92 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                                                                                                                  MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                                                                                                    assays to identify modulators of SP expression and activity. The anti-SP antibodies and antagonists may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The present sequence represents the amino acid sequence of a human secreted protein.
                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; anorectic; virucide; antibacterial; fungicide; protozoacide; mocropic; neuroprotective; antiparkinsonian; anticorropic; neuroprotective; antiparkinsonian; anticorropic; antiarthritic; antiinflammatory; dermatological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGFR4; complement factor I precursor; matrix metalloproteinase-15 precursor; MDC3; T-lymphocyte surface antigen Ly-9 precursor; fibroblast growth factor-21; FGF-21; alpha-2 macroglobulin-like polypeptide variant; anticlekoptoteinase 1 precursor; LiV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                                                                                    22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAMTSKTSVAXVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                                                  KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                                                                                                                   Gaps
                                                                                                                                                                                   ö
                                                                                                                                                 Length 329;
                                                                                                                                                                                   Indels
                                                                                                                                                  100.0%; Score 1039; DB 8;
100.0%; Pred. No. 6.7e-88;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL57243 standard; protein; 526 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NOV5c protein SEQ ID NO:188.
                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Ser, Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Glu, Lys
                                                                                                                                                                                                                                                                                                                                                                                                                    NSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2003; 2003WO-US028141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-2004 (first entry)
                                                                                                                                                                                      Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 489
                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                     Sequence 329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004022723-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                     202
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *
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TAONPVSNNSD-SISARQLCAD 193 183 TAONPVSORSSLPVHVGOFCTD 204

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119

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human; antidiabetic; anorectic; cardiant; hypotensive;
                                                                                                                                                                                                                                                                                                           Human NOV5b protein SEQ ID NO:50.
                                                                                                                                                                                                                     ADL57105 standard; protein; 526
                                                                                                                                                                                                                                                                               03-JUN-2004 (first entry)
                                                                                                                                                                                                                                                   ADL57105;
                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                          ADL57105
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                                                                                                                                            셤
                    a
                                                      ò
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                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequence fully defined in the generic form of any of the 37 amino acid sequence fully defined in the appetification. A polypeptide of the invention has antidiabetic, anorectic, cardiant, hypotensive, antiateriosclerotic, ancientification, antidonoulsant, obsteopathic, neuroprotective, antipatexhianory, dermatological, antiasthematic, and antibodies are useful in the manufacture of a medicament for triasthematic, and antibodies are useful in the manufacture of a medicament for triating asyndrome associated with a human disease, perferably a NOVA-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or disaponeing diseases such as metabolic disorders, clabeles, perventing or disaponeing diseases und antibodies are useful for treating, preventing or disaponeing diseases such as metabolic disorders, clabeles, perventing or disaponeing diseases und antibodies are useful for treating, preventing or disaponeing diseases und antibodies are useful for clabeles, polypeptides and antibodies are useful for creating, preventing or disaponeing diseases und antibodies are dispease, peripepy, immune disorders, inclementation, and protoxoal), ancoraxia, cancer, cardigovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders (osteoarthritis), heamatopoletic disorders, inflammatory skin disorders, costeoarthritis), heamatopoletic disorders, inflammatory skin disorders, in generation, haematopoletic disorders, inflammatory skin disorders, and particular disorders and antipolate are further used as hybridisation probes, in chromosome mapping, preventive medicine show homology to estimath factor receptor of regers in Novia-1c show homology to fibroblast growth factor-21 proteins; Novia-2 shows homology to alphabetic and part are propered by an antipolation of the invention show homology to certain knows homology to marix metalloproceanases; 
                                                                                                                                                                                                                                 New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                                              Rieger DK;
                                                                                                                                                                              Padigaru M,
                                                                                                                                                                                                                                                                                                               Example 5; SEQ ID NO 188; 214pp; English.
                                                                                                                                                                              Ort T,
                                                                                                                                                                              Guo X, Anderson DW,
                                                        23-SEP-2002; 2002US-0412766P.
23-SEP-2002; 2002US-0412825P.
24-SEP-2002; 2002US-0412767P.
25-SEP-2002; 2002US-0413342P.
              10-SEP-2002; 2002US-0409544P.
12-SEP-2002; 2002US-0410320P.
16-SEP-2002; 2002US-0411060P.
2002US-0409145P.
                                                                                                                      30-SEP-2002; 2002US-0414832P
                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                          WPI; 2004-315567/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated polypeptide (NOVX) comprising mature form of any of the 37 amino acid sequences fully defined in the specification. A polypeptide of the invention has antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide, antibacterial, fungicide, protozoacide, nootropic,
antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiniflammatory; fibroblast; growth factor receptor 4; FGRR4; complement factor I precursor; matrix metalloproteinase-15 precursor; fibroblast growth factor receptor 4; FGRR4; fibroblast growth factor-21; FGF-21; antialpha-2 macroglobulin-1ike polypeptide variant; alpha-2 macroglobulin-1ike polypeptide variant; antileukoproteinase 1 precursor; LIV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ort T, Padigaru M, Rieger DK;
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2002US-0412825P.
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2002US-0413342P.
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N-PSDB; ADL57104.
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24-SEP-2002;
25-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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12-SEP-2002;
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23-SEP-2002;
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1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTS-KTSVAYVTPGDSETAPVVTVTHRN 59

33.9%; Score 352; DB 8; Length 526; 38.1%; Pred. No. 8.4e-24;

14; Gaps

Indels

70;

41; Mismatches

Query Match
Best Local Similarity 38.14
Matches 77; Conservative

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autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome; gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis; osteoporosis, pancreatitis, tesiter's syndrome; rheumatoid arthritis, Sjogren's syndrome; uveitis, trauma, viral infection, bacterial infection; fungal infection; parasitic infection; protozoal infection; helminthic infection;

gene therapy; human

WO200272794-A2. Homo sapiens.

19-SEP-2002

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redroprocective, antinflammatory, antinflammatory, antiatchmatic, antinflammatory, antinflammatory, antiatchmatic, antinflammatory, antinflammatory, antinflammatory, antinflammatory, antinflammatory, antinflammatory, antinflammatory, antinflammatory, antilogueant for treating a syndrome are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases (viral, bacterial, fungal, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, epilepsy: immune disorders, Alzheimer's consecutrbritis), hasmatopoietic disorders, inflammatory skin disorders, asthma, and various dyslipidaemias. The nucleic acids and polypeptides or antibolise for the identification of small molecules therapy, in generation of antibodies that bind immunospecifically to Nova substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, trissue typing, preventive medicine, and pharmacogenomics. The NovX polypeptides of the invention show homology to certain known human croposities by the mology to fibroblast growth factor receptor (FGFR4); NOV2a shows homology to gibroblast growth factor: 1 precursor; NOV3a shows homology to alpha-2 macroglobulin-like contingent conting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor; NOV9-91 show homology to LIV-1 protein; NOV10a shows homology to nuclear hormone receptor NOR-1; NOV11a-11] show homology to transmembrane protein-like; NOV12a-12c show homology to beta-necendorphin precursor. The present sequence represents a NOVX polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT-Q 118
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neuroprotective, antiparkinsonian, anticonvulsant, osteopathic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 352; DB 8; Length 526;
; Pred. No. 8.4e-24;
41; Mismatches 70; Indels
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Query Match
Best Local Similarity 38.1.,
Best Local 77; Conservative
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New human immunoglobulin superfamily proteins and polynucleotides, useful for diagnosing, treating or preventing disorders with aberrant IGSFP expression, such as autoimmune, inflammatory or cell proliferative

Claim 1; Page 129-130; 145pp; English.

diseases

Yang J;

Thangavelu K, Warren BA, Tang YT, Duggan BM; nn MR, Honchell CD, Burford N, Forsythe IJ,

12-MAR-2001, 2001US-0275249P. 31-AUG-2001, 2001US-0316810P. 21-SEP-2001, 2001US-032977P. 25-OCT-2001, 2001US-03438447P. 02-NOV-2001, 2001US-0343880P.

(INCY-) INCYTE GENOMICS INC.

Baughn MR,

Mason PM;

Tran UK, Yue H,

Xu Y,

WPI; 2002-723340/78.

N-PSDB; ABS76363.

12-MAR-2002; 2002WO-US009052

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The present invention relates to new immunoglobulin superfamily proteins (IGSFP). The polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of IGSFP, particularly cell proliferative, e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal cocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thrombocytopenia or cancers including leukaemia, lymphoma, sarcoma or myeloma, and autoimmune or inflammatory disorders, e.g. acquired myeloma, and autoimmune or inflammatory disorders, e.g. acquired thyroiditis, contact dermatitis, Chan's disease, diabetes mellitus, thyroiditis, contact dermatitis, gondrome, gout, Graves' disease, clanamico's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, trauma, or viral, bacterial, arbitis, siggen's syndrome, uveitis, trauma, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections. They are also useful in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of IGSFP. The present compounds on the anino acid sequence represents a human IGSFP protein of the invention
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38.1%; Pred. No. 9e-24;
ive 41; Mismatches 70; Indels
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Immunoglobulin superfamily protein; IGSFP; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis; primary thrombocytopenia; cancer; leukaemia; lymphoma; sarcoma; myeloma; autoimmune disorder; inflammatory disorder;

Human immunoglobulin superfamily protein IGSFP-8.

(first entry)

11-DEC-2002

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SIMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEEGNVLQIFQTPEDQELTYTC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated immune response associated protein (IRAP) comprising any of 15 fully defined sequences given in the specification. The polypeptide of the invention demonstrates antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian, hepatotropic, cerebroprotective, antiinflammatory, nootropic and vasotropic activities and may be useful for treating a disease or condition associated with decreased expression or overexpression of functional immune response associated proteins, while the antibody is useful for diseases of condition or disease associated with the expensesion of likap, such as arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease and Crohn's disease. Furthermore, the molecules of the invention may be utilised during gene therapy procedures. The current sequence is that of a human IRAP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated immune response associated proteins (IRAP) polypeptide and polymucleotide, useful for diagnosing and/or treating disorders with aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ramkumar J, Swarnakar A, Elliott VS, Hafalia AJA, Richardson TW;
Lee SY, Lindquist EA, Marquis JP, Chawla NK, Khare R, Becha SD;
                                                                                                                                                                                                                                                                                                                                          immune response associated protein; IRAP; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; ecebroprotective; antiinflammatory; nootropic; vasciropic; arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease; Parkinson's; Crohn's; gene therapy; human.
                                                                                                                                                                                                                                                                                                              Human immune response associated protein IRAP-23 protein.
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                                                                        TAQNPVSNNSD-SISARQLCAD 193
                                                                                                        223 TAONPVSORSSLPVHVGOFCTD 244
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13-SEP-2002; 2002US-0410571P.
18-OCT-2002; 2002US-0419906P.
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N-PSDB; ADK98595.
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Length 565;

Score 352; DB 8; Pred. No. 9.3e-24;

33.9%; 38.1%;

Query Match Best Local Similarity

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                                                                     119 SLMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEEGNVLQIFOTPEDQELTYTC 172
                   59
                                1 KDSEIFTVNGILGESVTFPVNIQEPROVKIIAWTS-KTSVAYVTPGDSETAPVVTVTHRN
                                                          60 YYERIHALGENYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKFKIT-Q
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 Indels
70;
 41; Mismatches
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Search completed: February 4, 2005, 12:11:03 Job time : 90.3239 secs

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US-09-149-476-483
; Sequence 483, Application US/09149476
; Patent No. 6420526
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Sequence 483, App
Sequence 7327, Ap
Sequence 4, App
Sequence 4, Appli
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Appli
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-462-738-4

US-08-462-738-4

US-08-462-738-6

US-08-880-875-4

US-08-199-955-4

US-08-199-955-6

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US-08-348-792-8

US-08-348-792-8

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US-08-348-792-8

US-08-348-792-2

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sequence 6428, Application US/0949016

sequence 6428, Application US/0949016

rithe OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

rithe OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

rithe OF INVENTION: UNMBER: US/09/949,016

current Filing Date: 2000-04-14

prior Application NUMBER: 60/241,755

prior Filing DATE: 2000-10-20

prior Filing DATE: 2000-10-3

prior Filing DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2000-10-03

prior Filing DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

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100.0%; Pred. No. 1.2e-101;
ive 0; Mismatches 0;
US-09-199-955-10
US-08-880-875-10
US-09-513-999C-4353
US-09-369-248A-3
US-09-907-794A-320
US-09-907-794A-320
US-09-906-700-320
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US-09-906-63A-320
US-09-906-63A-320
US-09-906-63A-320
US-09-906-618-320
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US-09-949-016-6907
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Best Local Similarity 100.
Matches 199; Conservative
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GENERAL INFORMATION:

APPLICANT: Rosen et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1 APPLICATION NUMBER: US/09/149,476
FILING DATE: 1998-09-08
APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-07 CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER APPLICATION NUMBER: 60/040,606
EARLIER APPLICATION NUMBER: 60/040,607
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-03
EARLIER FILING DATE: 1997-03-03
EARLIER FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,581
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,584
R APPLICATION NUMBER: 60/047,500
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,587
R APPLICATION NUMBER: 60/047,587
R APPLICATION NUMBER: 60/047,492
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R APPLICATION DATE: 1997-05-23 R APPLICATION NUMBER: 60/047,582
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,596
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,612
R FILING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R R REPLICATION NUMBER: 60/047,632
R R RELING DATE: 1997-05-23
R R R R R PELICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/043,580
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R FILING DATE: 1997-04-11
R RAPLICATION NUMBER: 60/043,314
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,618

R FILING DATE: 1997-05-23

R PELING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,592

R PILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 EARLIER DE PRINTER DE PRINTER DE PRESENTER D EARLIER SARLIER SARLIER SARLIER SARLIER SARLIER

R APPLICATION NUMBER: 60/056,874
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,910
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22 R FILING DATE: 1997-06-06
R FILING DATE: 1997-08-06
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,877
R FILING DATE: 1997-08-22
R RAPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,599
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,588
FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,631 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22
APPLICATION WUMBER: 60/056,880
LILNG DATE: 1997-08-22
APPLICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION WUMBER: 60/056,882 ELING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 APPLICATION NUMBER: 60/056,879 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,761 APPLICATION NUMBER: 60/047,595 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,630 APPLICATION NUMBER: 60/056,878 APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 1997-08-22 997-08-22 FILING DATE: 1997-04-11 1997-08-22 1997-04-11 FILING DATE: 1997-04-11 1997-08-2 FILING DATE: FILING DATE: FILING DATE: FILING DATE: BARLIER
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FAREMAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 7327

SEQ ID NO 7327
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Pred. No. 1.2e-101;
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GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER PILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
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EARLIER PILING DATE: 1997-07-08
EARLIER PILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER APPLICATION NUMBER: 60/052,933
EARLIER APPLICATION NUMBER: 60/052,933
EARLIER PILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
US-09-949-016-7327; Sequence 7327, Application US/09949016; Patent No. 6812339
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Patent No. 6342581
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 199; Conservative
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US-09-949-016-7327
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US-09-227-357-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
        ER APPLICATION NUMBER: 60/047,586
ER FILING DATE: 1997-05-23
ER PLING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,594
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,589
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,614
ER FILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,614
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER PILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
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EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,887
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60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 206
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                                                                                                                                                                                                          30 VVAVLQESISLPLEIPPDEEVENIIWSSHKSLATVVPGKEGHPATIMVTNPHYQGQVSFL 89
                                                                                                                                                 8 VNGILGESVTFPVNIQEPROVKIJAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHAL
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APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: ADDRESS: ADDRESS: ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                   68 GPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGK 113
                                                                                                                                                                                                                                                                                                                    90 DPXYSLHISNLSWEDSGLYQAQVNLRTSQISTWQQYNLCVYRWLSE 135
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15.4%; Score 160; DB 1; Length 298;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels
                          Length 143
                                                                                  44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CALLUCAL
COUNTRY: USA
ZUP: 94304-1104
ZUP: 94304-1104
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-US44
FILING DATE: 02-DEC-US44
                   Query Match 17.5%; Score 182; DB 3; Best Local Similarity 35.8%; Pred. No. 2.1e-11; Matches 38; Conservative 24; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 LGESVTFP----VNIQEPRQVKIIAWTSKT---
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-348-792-4
; Sequence 4, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34.0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 298 amino acids
amino acid
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STATE: California
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OTHER INFORMATION: Xaa equals stop translation
.09-227-357-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/058,785
EARLIER PILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
                   R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,916

R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,930

R FILING DATE: 1997-07-08

R APPLICATION NUMBER: 60/051,918

R APPLICATION NUMBER: 60/051,918

R APPLICATION NUMBER: 60/051,920

R APPLICATION NUMBER: 60/051,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R APPLICATION NUMBER: 60/055,948
R FILING DATE: 1997-08-18
R APPLICATION NUMBER: 60/055,949
RR FILING DATE: 1997-08-18
R FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                       R FILING DATE: 1997-07-08

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R FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,932
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APPLICATION NUMBER: 60/055,723
FILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/055,684
FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,954
FILING DATE: 1997-08-18
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SEQ ID NO 192
LENGTH: 143
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ORGANISM: Homo sapiens
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LOCATION: (138)
OTHER INFORMATIC
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NAME/KEY: SITE
LOCATION: (143)
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NAME/KEY: SITE
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LOCATION: (136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Sequence 4, Application US/09199955
Patent No. 6372899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
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                                                                                                                                    Sequence 4 Application US/08462738

Patent No. 5977303

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Chia-chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Dan E.
TITLE OF INVENTION: SUBFACE ANTIGENS; PROTEINS AND ANTIBODIES
WUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%; Score 160; DB 2; Length 298; 25.4%; Pred. No. 1.4e-08; tive 35; Mismatches 78; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGRYT INFORMATION:
NAME: Ching, Edwin P: 74,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REJERRANICATION INFORMATION:
TELERDANICATION INFORMATION:
TELERDANICATION INFORMATION:
TELERDANICATION 150-2936
TELERDANICATION 150-2036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 YICTVSNPISNNSQTFS 223
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                         207 YICTVSNPISNNSQTFS 223
170 YTCTAQNPVSNNSDSIS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 25.4%
Matches 50; Conservative
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MOLECULE TYPE: protein
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                                                                                                             RESULT 6
US-08-462-738-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78; Indels 34; Gaps
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DARA Research Institute
STREET: 901 California Avenue
CUITY: Palo Alto
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.4%; Score 160; DB 3; Length 298; Best Local Similarity 25.4%; Pred. No. 1.4e-08; Matches 50; Conservative 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1104

ZIP: PABONABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PREM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-UNN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFERMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-880-875-4; Sequence 4, Application US/08880875; Patent No. 6399065; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 YICTVSNPISNNSQTFS 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 298 amino acids amino acid
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99 YLE------NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK 147
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Patent No. 5977303

GENERAL INFORMATION:
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Dan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                               PURIFIED GENES ENCODING MAMMALIAN CELL SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.4%; Score 160; DB 1; Length 305; Best Local Similarity 25.4%; Pred. No. 1.4e-08; Matches 50; Conservative 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                          STATE: CALLLILL
COUNTRY: USA
ZIP: 94304-1104
ZIP: 94304-1104
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN BATA: US/08/348,792
RILING DATE: 02-DEC-1994
CLASSIFICATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REFERRATION NUMBER: DX0436
TELEPOMMUNICATION INFORMATION:
TELEPOMMUNICATION INFORMATION:
TELEPAS. 415-452-9196
TELEPAS. 415-46-1200
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENGTH: 305 amino acids
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                                                                                                                                             TITLE OF INVENTION: PURIFIED GENES EN
TITLE OF INVENTION: SURFACE ANTIGENS;
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 YTCTAQNPVSNNSDSIS 186
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amino acid
GY: linear
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                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTRN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Gaps
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: PURIFIED GENES ENCODING MANMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: DNAX Research Institute
STREET: 91 California Avenue
CITY: Palo Alto
COUNTRY: USA
ZIP: 9410*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRICKATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-7UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436K
TELECOMMUNICATION INPORMATION:
TELEPHONE: 415-495-1200
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08348792;
Patent No. 557643;
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chita-Chun J.
APPLICANT: Chang, Chita-Chun J.
APPLICANT: Check, Benjamin G.
APPLICANT: de Vries, Jan E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 YTCTAQNPVSNNSDSIS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TOPOLOGY: 1:-cd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-880-875-4
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60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGPQHADNI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LGESVTFP-----VNIQEPRQVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN 59
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Patent No. 6399065

GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Jan E.
TITLE OF INVENTION: FURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.4%; Score 160; DB 3; Length 305; Best Local Similarity 25.4%; Pred. No. 1.4e-08; Matches 50; Conservative 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE:
CLASSIFICATION: 435
                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDAER:
APPLICATION NUMBER: 05 08/461,473
FILING DATE: 05-UNN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: DNAX Research Institute
901 California Avenue
                                                          APPLICATION NUMBER: US/09/199,955
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX. 415-496-1200
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 305 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-09-199-955-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DNAX Res
STREET: 901 Califor
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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US-08-880-875-6
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vies, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SUBFACE ANTIGENS: PROTEINS AND ANTIBODIES
TORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
15.4%; Score 160; DB 2; Length 305;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: DNAX Research Institute
901 Californía Avenue
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-199-955-6; Sequence 6, Application US/09199955; Patent No. 6372899; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 YTCTAQNPVSNNSDSIS 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 305 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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118 OSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169
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                                                                                                                                                                                                                                                                                                                                                                                                           12 LGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN
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Patent No. 5977303

GRERRAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: PUNIETED GENES ENCODING MAWMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                                                                                                                                                                                                                                               Length 307;
                                                                                                                                                                                                                                                                                                                            78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/462,738.
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            ; Score 160; DB 1;
; Pred. No. 1.4e-08;
35; Mismatches 78
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STREET: 901 California Avenue
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.4%;
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REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 307 amino acids
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                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-792-8
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Resect
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STATE: California
COUNTRY: USA
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US-08-462-738-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LGESVIFF-----VNIQEPRQVKIIAWISKT-----SVAYV PGDSETAPVVTVTRRN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08348792
Patent No. 5576423
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APRICANT: Cocks, Benjamin G.
APRESPONDENCE SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.4%; Score 160; DB 3; Length 305; Best Local Similarity 25.4%; Pred. No. 1.4e-08; Matches 50; Conservative 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACADERSEES: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: US-DEC-1994
CLASSIFICATION: 530
ATTONEY/AGENT INPORMATION:
NAME: CALING Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
RECENENCE/DOCKET NUMBER: JX080
TELECHONE: 415-495-1996
TELEPAX: 415-496-1200
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SEQUENCE CHARACTERISTICS:
LENGTH: 305 amino acids
                                                                                                                                                                                                                                                                                                   6 TYPE: amino acide TOPOLOGY: 11-
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US-08-348-792-8
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                                                                                                                                                                                                                                                                                                                                                            12 LGESVTPP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVTHRN 59
                                                                                                                                                                                                                                                                                                                                                                                                                 11 LGSKVLLPLTYBRINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 70
                                                                                                                                                                                                                                                                                       78; Indels 34; Gaps
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j Sequence 8, Application US/0919955

j Patent No. 6372899

j GENERAL INFORMATION:
   APPLICANT: Average Gregorio
   APPLICANT: Chang, Chia-Chun J.
   APPLICANT: Cocks, Benjamin G.
   APPLICANT: Cocks, Benjamin G.

                                                                                                                                                                                                      Query Match
15.4%; Score 160; DB 2; Length 307;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: 08/461,473
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 YTCTAQNPVSNNSDSIS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YICTVSNPISNNSQTFS 195
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
trPE: amino acid
; TOPOLOGY: linear
; MOLECTUE TYPE: protein
US-08-462-738-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-199-955-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-199-955-8
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Query Match
Best Local Similarity 25.4%; Score 160; DB 3; Length 307;
Best Local Similarity 25.4%; Pred. No. 1.4e-08;
Matches 50; Conservative 35; Mismatches 78; Indels 34; Gaps 8;

Qy 12 LGESVTFP----VNIQEPROVILIANTST-----SVAXVTPGDSETAPVYTVTHRN 59
11 LGSKULLPLTYERINKSMNKSIHIVVTMAKSLENSVENKIVSLDPSEAGPPRYLGDRYKF 70

Qy 60 YYERIHALGPNYNLYISDLRMEDGDYKADINTQADPYTTTRRYNLQ--IYRRLGKPKIT 117

Db 71 YLE-----NLTLGIRESRREDEGWYLMT----EKNVSVQRFCLQLRLYEQVSTPEIK 119

Qy 118 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169

Db 120 VLNKTQENGTCTLILGCTVEKGD-HVAYSWSEKAGTHPLNPANSSHLLSLTLGFQHADNI 178

Qy 170 YTCTAQNPVSNNSDSIS 186

Qy 170 YTCTAQNPVSNNSDSIS 186

Db 179 YICTYSNPISNNSQTFS 195

Search completed: February 4, 2005, 12:17:04
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February 4, 2005, 12:15:12; Search time 65.5796 Seconds (without alignments) 988.338 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                          US-09-882-171-483_COPY_22_220
1039
1 KDSEIFTVNGILGESVTFPV.......NNSDSISARQLCADIAMGFR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/prodatea/2/pubpaa/US07_PUBCCMB.pep:*

2: /cgn3_6/prodatea/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/prodatea/2/pubpaa/NEG_NEW_PUB.pep:*

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18: /cgn2_6/prodatea/2/pubpaa/US10_PUBCCOMB.pep:*

19: /cgn2_6/prodatea/2/pubpaa/US10_PUBCCOMB.pep:*

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19: /cgn2_6/prodatea/2/pubpaa/US60_PUBCCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Sequence 4, Appli Sequence 30, Appl Sequence 483, App Sequence 483, App Sequence 483, App Sequence 89, Appli Sequence 8, A Sequence 1, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 79, Sequence 77, Description US-10-104-943-4 US-10-46-523-30 US-09-809-391-483 US-09-809-171-483 US-10-164-861-483 US-10-164-861-483 US-10-104-943-7 US-10-328-538-2 US-10-328-538-2 US-10-436-523-92 100 110 110 110 110 110 110 110 Query Match Length DB 100.0 100.0 100.0 100.0 100.0 133.9 133.9 133.1 133.1 132.0 12.0 1039 1039 1039 1039 1039 352 343.5 343.5 343.5 332 332 No.

Sequence 18, Appl	76,	89,	91, A	131,	88,	90,	4	16,	ທີ	Sequence 2, Appli	'n	2559	22,	76,	Ē	76,	76,	76,	7	76,	76,	76,	76,	76,			16,	76,	e 76,	Sequence 76, Appl	e 76,	
-10		US-10-436-	US-10-436-	5 US-10-170-385-131	US-10-436-	US-10-436-		ĭ	US-10-4	US-10-	ĭ	ï	-614-	-245-	4 US-10-245-859-76	-242-	-242-	4 US-10-245-143-76	US-10-245-	1-245-	US-10-245-)-237-	3-238-18	0-238-	0-238-37	4 US-10-245-055-76	0-245-	**	4 US-10-245-739-76	4 US-10-246-210-76	4 US-10-239-196-76	
289 1	1	6	6	4	1	-	285 1	203 1	9	331	331 1	331 1	331 1	332 1	332 1	332 1	332	332 1	332 1	332 1	332 1	332 1	332 1	332 1	332 1	332 1	3	m	33	332 1	332 1	
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ALIGNMENTS

RESULT 1 US-10-104-943-4 US-10-104-943-4 SUBJUCTATION ON US20030092017A1 SUBJUCTATION NO. US20030092017A1 GENERAL INFORMATION: APPLICANT: BRISTOL—WAYER SQUIDD COMDANY TITLE OF INVENTION: DOLYNUCLEOTIDE ENCODING A NOVEL IMMUNOGLOBULIN SUPERFAMILY MEMBE TITLE OF INVENTION: DATA: 2002-03-22 CURRENT FILING DATE: 2002-03-22 PRIOR FILING DATE: 2001-04-03 PRIOR FILING DATE: 2001-04-03 PRIOR FILING DATE: 2001-04-03 SOFTWARE: Patentin version 3.0 SEQ ID NO 4 LENGTH: 328 TYPE: PRY CRANISM: HOMO Sapiens US-10-104-943-4	NOVEL IMMUNOGLOBULIN SUPERFAMILY MEMBE VARIANTS THEREOF
Query Match 100.0%; Score 1039; DB 14; Len Best Local Similarity 100.0%; Pred. No. 3.8e-89; Matches 199; Conservative 0; Mismatches 0; Inde	DB 14; Length 328; 1e-89; 0; Indels 0; Gaps 0;
Qy 1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY	
Db 22 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAMTSKTSVAYVTPGDSETAPVVTVTHRNY	SKTŠVAÝVTPGDSETAPVVTVTHRNY 81
Qy 61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120	NDPYTTKRYNLQIYRRLGKPKITQSL 120
Db 92 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141	ADPYTTKRYNLÖIYRRIGKPKITOSL 141

121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180

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Appli Appli Appli Appli Appl

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FILING DATE:
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US-09-882-171-483
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61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                             APPLICANT: Fraeer, Christopher C.
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
FILE REFERENCE: 7853-244-999
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT FILING DATE: 2003-05-12
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR PILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1039; DB 14; Length 328; llarity 100.0%; Pred. No. 3.8e-89; Conservative 0; Mismatches 0; Indels 0;
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Sequence 483, Application US/09809391

Sequence 483, Application US/09809391

Publication No. US20030049618A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: PZ002100

CURRENT APPLICATION NUMBER: US/09/809,391

CURRENT FILING DATE: 2001-03-16

PHIOR APPLICATION NUMBER: US/09/809,391

CURRENT FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 761

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NOS 483

LENGTH: 329
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FRATURE:
INAME/KEY: SITE
I. LOCATION: (329)
CHER INFORMATION: Xaa equals stop translation
US-09-09-391-483
                                                                                                                                                                              Sequence 30, Application US/10436523
Publication No. US20030180888A1
GENERAL INFORMATION:
                                                                             202 NSDSISAROLCADIAMGFR 220
                                                      181 NSDSISARQLCADIAMGFR 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 199; Conserv
                                                                                                                                                               US-10-436-523-30
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61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 MASVNSTCNVTLTCSVEKBERNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 201
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                                                                                                                                               1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
                                                                                      Gaps
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              DB 10; Length 329;
                                                                               Indels
       100.0%; Score 1039; DB 10;
100.0%; Pred. No. 3.8e-89;
ive 0; Mismatches 0;
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THILE OF INVENTION: 186 Human Secreted proteins
THILE OF INVENTION: 186 Human Secreted proteins
THILE OF INVENTION: 186 Human Secreted proteins
THILE SPERENCE: P2002P2
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR PLING DATE: 1998-03-06
PRIOR PLING DATE: 1998-03-06
PRIOR PLING DATE: 1998-03-07
PRIOR PLING DATE: 1997-03-07
PRIOR PPLICATION NUMBER: 60/040, 336
PRIOR PLING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040, 163
PRIOR PRIOR DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040, 163
PRIOR APPLICATION NUMBER: 60/040, 163
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NR FILING DATE: 1997-05-23
NR APPLICATION NUMBER: 60/047,615
OR FILING DATE: 1997-05-23
OR APPLICATION NUMBER: 60/047,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 483, Application US/09882171; Publication No. US20030175858A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION UNMBER: 60/047,592
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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Query Match
Best Local Similarity 100.
Matches 199; Conservative
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PRIOR FILING DATE: 1997-05-23

PRIOR PLING DATE: 1997-06-11

PRIOR PLING DATE: 1997-04-11

PRIOR PLING DATE: 1997-06-22

PRIOR

PRIOR APPLICATION NUMBER: 60/056,819
PRIOR PLILING DATE: 1997-08-2
PRIOR APPLICATION NUMBER: 60/056,911
PRIOR APPLICATION NUMBER: 60/056,910
PRIOR PLILING DATE: 1997-08-2
PRIOR APPLICATION NUMBER: 60/056,912
PRIOR PLILING DATE: 1997-08-2
PRIOR APPLICATION NUMBER: 60/047,589
PRIOR PLILING DATE: 1997-06-2
PRIOR

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JS-09-860-836B-11
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                                                                                                                                                                                                                                                                                                                                           121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
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                                                                                                                 DB 10; Length 329;
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                                                                                                       100.0%; Score Luss; --
100.0%; Pred. No. 3.8e-89;
+ive 0; Mismatches 0;
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Sequence 483, Application US/10164861
FUDLication No. US2030225248A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILL OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILLING DATE: 2002-06-10
FRIOR APPLICATION NUMBER: US/09/149,476
FRIOR APPLICATION NUMBER: US/09/149,476
FRIOR APPLICATION NUMBER: PCT/US98/04493
FRIOR PLING DATE: 1998-09-08
FRIOR PLING DATE: 1998-03-06
NUMBER: OF SEQ ID NOS: 757
SOFTWARE: PATENTIN DATE: 2096-206
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100.0%; Score 1039; DB 15
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 199; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05
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                                                                                                             Query Match
Best Local Similarity 100.(
Matches 199; Conservative
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FEATURE:
NAME/KEY: SITE
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LENGTH: 329
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163 SVKVSENFSCNITLMCSVKGAEKSVLYSWTPREPHASESNGGSILTVSRTPCDPDLPYIC 222
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Publication No. US20030054002A1
GENERAL INFORMATION:
APPLICANT: WAKELAND, WARD
APPLICANT: WANDSTRADT, AMY
APPLICANT: MOREL, LAURENCE
TITLE OF INVENTION: IN IMMUNE TOLERANCE
FILLE REFERENCE: UTSD: 722US
CURRENT APPLICATION NUMBER: US/09/860,836B
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                                                                                                                        APPLICANT: YUE, Henry; XU, Yuming;
APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
APPLICANT: TANG, Y. TON; DUGGAN, Brendan M.;
APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
APPLICANT: FONCHELL, Cynthia D.; BURFORD, Neil;
APPLICANT: FORSYTHE, Tan J.; YANG, Junming;
APPLICANT: MASON PERTICIA M.
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REPERENCE: PF-0925 USN
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33.9%; Score 352; DB 15;
Best Local Similarity 38.1%; Pred. No. 2.6e-24;
Matches 77; Conservative 41; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/471,449
CURRENT PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: PCT/US02/09052
PRIOR PILING DATE: 2002-03-12
PRIOR PLICATION NUMBER: US 60/275,249
PRIOR PILING DATE: 2001-03-12
PRIOR PLICATION NUMBER: US 60/316,810
PRIOR PLILING DATE: 2001-08-31
PRIOR PLILING DATE: 2001-08-31
PRIOR PLILING DATE: 2001-08-31
PRIOR PLILING DATE: 2001-09-21
PRIOR PELICATION NUMBER: US 60/348,447
PRIOR PLILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-11-02
PRIOR PELICATION NUMBER: US 60/348,447
PRIOR PELING DATE: 2001-11-02
PRIOR FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PERL PROGRAM
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; NAMB/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7500099CD1
US-10-471-449-8
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US-10-471-449-8
; Sequence 8, Application US/10471449
; Publication No. US20040097711A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 2, Application US/10310612;
Publication No. US20040109862A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of cells
TITLE OF INVENTION: that express Ly-9
TITLE REFERENCE: THE REFERENCE: US/10/310,612
CURRENT APPLICATION NUMBER: US/10/310,612
CURRENT FILING DATE: 2002-12-04
NUMBER: OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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Publication No. US20040109863A1
GENERAL INFORMATION:
APPLICANT: Entage, Peter
TITLE OF INVENTION: Methods of therapy and difference of therapy and the express Ly-9
TITLE REFERENCE: HYS-68CP
CURRENT APPLICATION NUMBER: US/10/328,538
CURRENT FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 AQNPVSQRSSLPVHVGQFCTD 243
            223 AQNPVSQRSSLPVHVGQFCTD 243
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Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Conservative
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Sequence 7, Application US/2003092017A1
Sequence 7, Application No. US2003092017A1
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF
TITLE OF INVENTION: and VARIANTS AND SPLICE VARIANTS THEREOF
FILE REFERENCE: D013-502-03-22
PRIOR APPLICATION NUMBER: US 60/278,037
PRIOR APPLICATION NUMBER: US 60/278,037
PRIOR APPLICATION NUMBER: US 60/281,223
PRIOR PILING DATE: 2001-04-03
PRIOR SEQ ID NOS: 129
NUMBER OF SEQ ID NOS: 129
NUMBER PRICE PATENTING NOS: 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 SVKVSENFCNITLMCSVKGAEKSVLYSWTPREPHASESNGGSILTVSRTPCDPDLPYICT 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 YYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKIT-Q 118
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                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                        Query Match 33.9%; Score 352; DB 10; Length 610; Best Local Similarity 38.1%; Pred. No. 3e-24; Matches 77; Conservative 41; Mismatches 70; Indels 1
PRIOR APPLICATION NUMBER: 60/204,963
PRIOR PILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAQNPVSQRSSLPVHVGQFCTD 213
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Best Local Similarity 36.84
Matches 74; Conservative
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                                                                                                                                                                                                           ORGANISM: Homo sapien
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68 GPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNST 127
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                                                                                                                                                                                              30 VVAVLQESISLPLEIPPDEEVENIIWSSKKSLATVVPGKEGHPATIMVTNPHYQGQVSFL
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Squence 77, Application US/10436523

Publication No. US20030180888A1

GENERAL INFORMATION:

APPLICANT: Fraser, Christopher C.

TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

FILE REFERENCE: 7853-244-999

CURRENT APPLICATION NUMBER: US/10/436,523

CURRENT FILING DATE: 2003-05-12

PRIOR APPLICATION NUMBER: US/10/007,303

PRIOR APPLICATION NUMBER: 09/706,167

PRIOR FILING DATE: 2000-11-03

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin version 3.1

SEQ ID NO 77
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9
                                                                                       Length 236;
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                                                                                       Query Match 32.0%; Score 332; DB 14; Best Local Similarity 38.1%; Pred. No. 6.4e-23; Matches 69; Conservative 37; Mismatches 69;
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32.0%; Score 332; DB 14;
Best Local Similarity 38.1%; Pred. No. 7.7e-23;
Matches 69; Conservative 37; Mismatches 69;
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US-10-220-946-18
Sequence 18, Application US/10220946
Publication No. US20030124575A1
GENERAL INFORMATION:
                             ORGANISM: Homo sapiens
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US-10-436-523-77
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        TYPE: PRT
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                                                                                       68 GPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNST 127
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                                                           120 IMASVNSTCNVTLTCSVEKEEKNVTYNWSPL-----GEEGNVLQIFQTPEDQELTYTCT
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US-10-436-523-79
Sequence 79, Application US/10436523
Fublication No. US20303018088A1
GENERAL INFORMATION:
APPLICANT: FRASEY. Christopher C.
TITLE OF INVENITON: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
FILE REFERENCE: 7853-244-999
CURRENT FILLON NUMBER: US/10/436,523
CURRENT FILLON DATE: 2003-05-12
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR PLING DATE: 2001-11-20
PRIOR PLING DATE: 2001-11-03
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 82, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION.
; APPLICATION NO. US2003018088A1
; TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
; FILE REFERENCE: 7853-244-99
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/007,303
; PRIOR APPLICATION NUMBER: 09/706,167
; PRIOR PILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 100
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
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32.0%; Score 332; DB 14;
Best Local Similarity 38.1%; Pred. No. 5.7e-23;
Matches 69; Conservative 37; Mismatches 69;
                                                                                                                                             174 AQNPVSNNSD-SISARQLCAD 193
                                                                                                                                                                                 223 AONPVSORSSLPVHVGOFCTD 243
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CORGANISM: Homo sapiens
US-10-436-523-79
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Sequence 76, Application US/10436523
Fubblication No. US20030180888A1
GENERAL INFORMATION:
TITLE OF INVERTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
TITLE OF INVERTION TORS-244-99
CURRENT APPLICATION NUMBER: US/10/436,523
FRIOR PELING DATE: 2003-05-12
FRIOR PELING DATE: 2001-120
FRIOR APPLICATION NUMBER: 09/706,167
FRIOR APPLICATION NUMBER: 09/706,167
FRIOR PILING DATE: 2000-11-03
FRIOR FILING DATE: 2000-11-03
SPROR FILING DATE: 2000-11-03
SOFTWARE: PARENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.0%; Score 332; DB 14; Length 289; Best Local Similarity 38.1%; Pred. No. 8.4e-23; Matches 69; Conservative 37; Mismatches 69; Indels
                                                                                                                  APPLICANT: JAILLAL
APPLICANT: Lapp, Hilmar
APPLICANT: Kalthoff, Frank Stephan
ITILE OF INVENTION: Organic Compounds
FILE REFERENCE: 4.31347 PCT
CURRENT FILING DATE: 2002-09-06
CURRENT FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/205,020
PRIOR APPLICATION NUMBER: US 60/205,020
PRIOR APPLICATION NUMBER: US 60/205,769
PRIOR APPLICATION NUMBER: US 60/205,769
PRIOR FILING DATE: 2000-05-19
  US20030124575Alartis AG
No. US20030124575/
No. US2003012457/
Phares, William
Werner, Gudrun
                                                                                                            Markus
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ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapiens
US-10-220-946-18
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US-10-436-523-76
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LENGTH: 289
                                                                             APPLICANT:
APPLICANT:
APPLICANT:
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32.0%; Score 332; DB 14; Length 289;

Query Match

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_79:*

e: pIR_79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES *

Description	LV-9.2 antiden - m	10	antigen BCM1 precu	signaling lymphocy	biliary glycoprote		biliary glycoprote		biliary glycoprote	nonspecific cross-	limbic-system-asso			biliary glycoprote	transmembrane carc	biliary glycoprote	opioid-binding pro		opioid-binding pro	opioid-binding cel	50K glycoprotein p	neurotrimin - rat	embryoni	T-cell surface gly	cell-adhesion mole	T-cell surface gly	pregnancy-specific	noeu	gene 2B4 protein -
. QI	A46500	801299	JL0143	\$58892	WMMSR1	JC1508	S34338	A36319	JC1509	A27681	JC4776	JH0395	JH0396	JH0394	C30127	A32164	JC1238	803199	JC1239	JC4025	JC5519	156551	A55811	S41638	S23969	RWHUC2	JC4123	A34815	149443
DB	~	•	~	7	-	7	7	~	~	7	~	7	~	~	~	Н	7	7	~	~	~	7	7	7	~	٦	7	~	~
Length	629	240	240	335	458	521	521	702	458	344	338	321	351	417	464	526	338	345	345	345	338	344	265	347	458	351	419	349	398
Query Match	28.4		15.9	15.4	13.4	13.4	13.1	13.0	12.7	12.7	12.0	11.8	11.8	11.8	11.8	11.8	11.7	11.7	11.7	11.6	11.5	11.5	11.4	11.4	11.1	10.9	10.9	10.6	10.6
Score	295	174	165.5	160	139	139	136	135.5	132	131.5	125	122.5	122.5	122.5	122.5	122.5	121.5	121.5	121.5	120.5	119.5	119	118	118	115.5	113.5	113.5		110
Result No.		1 73	ю	4	Ŋ	v	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

poliovirus recepto	biliary glycoprote	carcinoembryonic a	leukocyte antigen	C-CAM2a protein is	ecto-ATPase precur	neural cell adhesi	pregnancy-specific	pregnancy-specific	pregnancy-specific	elastic titin - hu	connectin 3B - chi	connectin/titin -	pregnancy-specific	pregnancy-specific	pregnancy-specific
JC4024	148268	A28333	A53244	568177	A44783	T43027	A28277	A33258	B33258	138346	PN0568	T42633	G43354	F43354	A43354
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518	272	286	243	458	519	1232	417	419	426	7962	1323	4162	324	326	333
10.6	10.4	10.3	10.3	10.3	10.3	10.3	10.1	10.1	10.1	10.1	9.9	9.9	9.8	9.8	9.6
110 10.6	108 10.4			106.5 10.3										102 9.8	

ALIGNMENTS

RESULT 1 A46500 Ly-9.2 antigen - mouse CySpecies: Wus musculus (house mouse) CySpecies: Was musculus (house mouse) CyAccession: A46500 CyAccession: A46500 Ay Title: Isolation and characterization of cDNA clones for mouse Ly-9. Ay Title: Isolation and characterization of cDNA clones for mouse Ly-9. Ay Reference number: A46500 Ay Status: preliminary Ay Molecule type: mRNA; protein Ay Residues: 1-629 < SAN> Ay Cross-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932 Ay Experimental source: CSTBL/6 Ay Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654) Cy Keywords: transmembrane protein
Query Match Best Local Similarity 34.9%; Pred. No. 6.1e-17; Matches 67; Conservative 31; Mismatches 88; Indels 6; Gaps 1;
QY 7 TVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHA 66
Qy 67 LGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLWASVNS 126 :
OY 127 TCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
Qy 181 NSDSISARQLCA 192 bb 414 SSSQFSSGTICS 425
RESULT 2 S01299 OX-45 membrane glycoprotein precursor - rat N;Alternate names: MRC OX-45 antigen N;Alternate names: MRC OX-45 antigen N;Alternate names: RRC OX-45 antigen C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004 C;Accession: S01299 R;Killeen, N.; Mosesner, R.; Arvieux, J.; Willis, A.; Williams, A.F. EMBO J. 7, 3087-31991, 1898 B,Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the A;Reference number: S01299; MUID:89030603; PMID:3181129

```
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-217/Product: antigen BCM1 #status predicted <NAT>
F;218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F;32,38,70,136,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                      128
                                                                                                                                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                 203
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                                                                                                                            Matches
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A;Cross-references: UNIPROT:P10252; EMBL:X13016; NID:956804; PIDN:CAA31438.1; PID:956805

A;Cross-references: UNIPROT:P10252; EMBL:X13016; NID:956804; PIDN:CAA31438.1; PID:956805

C;Superfamily: B-cell surface glycoprotein; predicted antigen

B;1-22/Domain: signal sequence #status predicted <SIG>
F;23-240/Product: OX-45 membrane glycoprotein #status predicted <MAT>
F;38,97,140,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse BCM1 (OX45 or Blast-1)
                                                                                                                                                                          9
                                                                                                                                                                                                                                                                RNYYERIHALGPNYNLVISDLRMEDAGD-YKADINTQADPYTTTKRYNLQIYRRLGKPKI 116
                                                                                                                                                                                                                                                                                                                            TQSLMASVNSTCNVTLICSVEKEEKAVTYNW-----SPLGEEGNVLQIFQTPEDQELTY 170
                                                                                                                                                                                                                                                                                                                                                134 KIEKTKNLTDSCHIRLSCKV--BDQGVDYTWYEDSGPFPQRNPGYVLEITITPHNKSTFY 191
                                                                                                                                                                                                                                      77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen BCM1 precursor - mouse
NyAlternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0143; S21319; A47469; B47469
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
J. Exp. Med: 171, 2115-2130, 1990
A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or
                                                                                                                                                                                                   1 KDSEIFTVNGILGESVTFPVNIQEPROVKIIAW---TSKTSVAYVTPGDSETAPVVTVTH 57
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                        22;
                                                                                                                                    16.7%; Score 174; DB 2; Length 240;
.larity 26.2%; Pred. No. 2.6e-07;
Conservative 36; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             TCTAQNPVSNNSDSI 185
                                                                                                                                                    Local Similarity
nes 51; Conserv
                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                           171
                                                                                                                                      Query Match
                                                                                                                                                      Best Loc
Matches
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A,MOlecule type: mRNA
A,Residues: 1-335 <COC>
A,Cross-references: UNIFROT:Q13291; EMBL:U33017; NID:g984968; PIDN:AAA75380.1; PID:g9849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: carcinoembryonic antigen mmCGMla, murine hepatitis virus receptor C;Species: Mus musculus (house mouse)
C;Species: Musmus-1993 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: JCISO5, A49006; A41563; S11625
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNVTLICSVEKEEKNVTYNW-----SPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSNN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 YYBRIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQ--IYRRLGKPKIT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 QSLMASVNSTCNVTLTCSVEKEEKNVTYNWS-----PL--GEEGNVLQIFQTPEDQELT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signaling lymphocytic activation molecule - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S58892
R;CocKs, B.G., Chang, C.C.; Carballido, J.M.; Yssel, H.; de Vries, J.B.; Ave Nature 376, 260-263, 1995
A;Title: A novel receptor involved in T-cell activation.
A;Reference number: S58892; MUID:95342241; PMID:7617038
A;Accession: S58892
A;Accession: S58892
                                                                                                                                                                                                                                                                                                                                              31 INATTGSNVTLKIHKDPLGPYKRITWLHTKNQKILEYNYNSTK---TIFESEFKGRVYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | | | | | | | | | | | | | | ENNGALHISNVRKEDKGTYYMRVLRETE---NELKITLEVFDPVPKPSIEINKTEASTDS
                                                                                                                                                                                                                                                    8 UNGILGESUTFPUNIQEPRQUKIIAWTSKTSVAYUTPGDSETAPVUTVTHRNYYERIHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLE-----NLTLGIRESRKEDEGWYLMTL----EKNVSVQRFCLQLRLYEQVSTPEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LGESVTFP-----VNIQEPROVKIIAWTSKT-----SVAYVTPGDSETAPVVTVHRN
            DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.4%; Score 160; DB 2; Length 335;
                                                                                                                                Indels
                                                                                                                          92;
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15.9%; Score 165.5; DB 2 24.2%; Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 6e-06; 35; Mismatches
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biliary glycoprotein A precursor - mouse
                                                                                                                          40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDSISARQLCADIA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 25.4%
Matches 50; Conservative
                                                                                                                                Conservative
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N;Alternate names: biliary glycoprotein 1
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1508; S65940; S36852
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopromy, Reference number: JC1505; MUID:93273228; PMID:8500759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, MOLECULE LYDE: MRNA
A, Residues: 1-521 < MNC-
A, Cross-references: UNIPROT: P31809; EMBL:X67279; NID:g50170; PIDN:CAA47696.1; PID:g50171
A, Experimental source: strain CD1; tissue colon
R, Nedellec, P.; Turbide, C.; Beauchemin, N.
R, Nedellec, P.; Turbide, C.; Beauchemin, N.
Bur. J. Blochem. 231, 104-114, 1995
A, Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A, Reference number: S65939; MUID:95354678; PMID:7628460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Scaus: translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Fosidues: 1-21 < NBD>
A,Cross-references: BMBL:X84054; NID:g1039337
A;Experimental source: strain BALB/c
A,Experimental source: strain BALB/c
A,Mode: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A,Note: only a part of the coding sequence is given
C,Comment: This protein is expressed at the cell surface and plays a determinant role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin C.Superfamily: carcinoembryonic transmembrane protein C.Keywords: glycoprotein; receptor; transmembrane protein P;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN> P;160-219/Domain: immunoglobulin homology <IMM1> P;254-303/Domain: immunoglobulin homology <IMM2> P;339-396/Domain: immunoglobulin homology <IMM3> P;71,89;104,148,199,206,210,226,258,280,294;304,317,333,375/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534338
biliary glycoprotein F - mouse
biliary glycoprotein F - mouse
biliary glycoprotein
NyAlternate names: mouse hepatitis virus (MHV) receptor glycoprotein
NyAlternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: S34338; JG1510; A41093
C;Accession: S34338; JG1510; A41093
A;Huang, X.F; Novel, M.; Novel, G.
Bubmitted to the EMBL Data Library, July 1992
A;Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A;Reference number: S34338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 KNVTYNWSPLGE-----EGN-VLQIFQTPEDOELTYTCTAQNPVS-NNSDSIS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 PRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY----YERIHALGPNYNLVISDLRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 22;
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27.4%; Pred. No. 0.00061;
tive 22; Mismatches 86
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Matches 49; Conservative
                                                                   D - mouse
                                                                   glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: 1458 a MCA.
A; Residues: 1-458 a MCA.
A; Roseler extracted from NCBI backbone (NCBIN:109445, NCBIP:109446)
A; Croseler extracted from NCBI backbone (NCBIN:109445, NCBIP:109446)
B; Dveksler, G.S.; Pensiero, M.N.; Cardellichio, C.B.; Williams, R.K.; Jiang, G.S.; Holme
J. Virol. 65, 6801-6801, 1991
A; Title: Cloning of the mouse hepatitis virus (MHV) receptor: expression in human and ha
A; Reference number: A41563
A; Accession: A41563
A; Accession: A41563
A; Accession: A41563
A; Residues: 1-458 a NUD:9194002; PIDN:AAA37858.1; PID:9194003
B; Beauchemin, N.
Bubmitted to the EMBL Data Library, May 1990
A; Reference number: S11626
A; Accession: S11626
A; Residues: 'PQ' 82-458 a BBA.
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A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprd A;Reference number: JC1505; MUID:93273228; PMID:8500759 A;Accession: JC1505 A;Accession: JC1505 A;Status; nucleic acid sequence not shown
                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-458 <MCC>
A;Crosteneces: 1-658 <MCC>
A;Ccualg, K.; Turbide, C.; Beauchemin, N.
Cell Growth Differ. 3, 165-174, 1992
A;Title: mmCGMlai a mouse carcinoembryonic antigen gene family member, generated by alte
A;Reference number: A49006; MUID:92338096; PMID:1633107
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A.77itle: A mouse analogue of the human carcinoembryonic antigen.
A.77itle: A mouse analogue of the human carcinoembryonic antigen.
A.77itle: A mouse analogue of the human carcinoembryonic antigen.
A.77itle: A mouse analogue of the human carcinoembryonic antigen.
A.77itle: S. 18625
A.77itle: A mouse analogue of the human carcinoembryonic antigen.
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Best Local Similarity
Matches 49; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: L22 cHUDA
A;Molecule type: L22 cHUDA
A;Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g312
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

A; Accession: S34338

---EGN-VLQIFQTPEDQELTYTCTAQNPVS-NNSDSIS 186

141 KNVTYNWSPLGE-

174 DNINYLWSRNGESLSEGDRLKLSEGNRTLTLLNVTRNDTGPYVČETRNPVSVNRSDPFS 232

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A;Gene: GDB:CEA
A;Cross-references: GDB:119054; OMIM:114890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S31737
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <BA2>
A;Cross_references: EMBL:X62151
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: S08106
A;Accession: S08106
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A; Residues: 5-702 <OIK>
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NyAlternate names: CEA, meconium antigen 100
Cippedies: Homo sapatens (man)
Cippedies: Homo sapatens (man)
Cippedies: Homo sapatens (man)
Cippedies: Homo sapatens (man)
Cippedies: His Thompson, J. Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shively, Mol. Cell. Biol. 10, 2738-2748, 1990
A; Reference number: A36319; MUID: 90258861; PMID: 2342461
A; Reference number: A36319; MUID: 90258861; PMID: 2342461
A; Residues: Homo sapatens (man)
A; Residues: L.J.C. & Complete gene for carcinoembryonic antigen: analysis of its prom A; Residues: L.J.C. & Complete gene for residue 641-Phe and CAG for residue 646-Thr Mol. Cell. Biol. 7, 3221-3230, 1987
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
Mol. Cell. Biol. 7, 3221-3230, 1987
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
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A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
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A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Commoyer, D.; Fuks, A.; Stanners, C.P.
A; Residues: L.J.C. & Co
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           of mouse colon biliary glycopro
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                                                                                                                                                                                                                                                                                              the carcinoembryonic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and plays a determinant role
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- EGN-VLQIFQTPEDQELTYTCTAQNPVS-NNSDSIS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: glycoprotein; receptor F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal hu F:1-138/Domain: immunoglobulin homology <IMM2>
F:254-303/Domain: immunoglobulin homology <IMM2>
F:339-396/Domain: immunoglobulin homology <IMM3>
F:319-396/Domain: immunoglobulin homology <IMM3>
F:319-396/Domain: immunoglobulin homology <IMM3>
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A;Title: Expression of the Bgp gene and characterization A;Reference number: JC1505; MUID:93273228; PMID:8500759 A;Accession: JC1510
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 35-59 <WIL>
C;Comment: This protein is expressed at the cell surface
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                                                                                                    A; Molecule type: mRNA
A; Residues: 1-81, 'Q', 83-141, 'P',143-521 <MCC>
A; Residues: 1-81, 'Q', 83-141, 'P',143-521 <MCC>
A; Cross references: GS, 875281
R; Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A; Title: Receptor for mouse hepatitis virus is a member A; Reference number: A41093; MUD:91288498; PMID:1648219
A; Scatus: preliminary
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C, Superfamily: carcinoembryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.8%
Matches 48; Conservative
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A; Molecule type: mRNA
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A/Residues: 1-102 cMAS.
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A;Map position: 19913.2-19913.2

A;Map position: 19913.2-19913.2

C;Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termin c;Superfamily: carcinoembryonic antigen, carcinoembryonic antigen, carcinoembryonic antigen precursor amino-terminal blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat; F;1-134/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEAN> F;1-34/Domain: signal sequence #status predicted cSIS>
F;1-34/Domain: signal sequence #status predicted cSIS>
F;1-60-217/Domain: immunoglobulin homology cIMM1>
F;252-3101/Domain: immunoglobulin homology cIMM2>
F;252-301/Domain: immunoglobulin homology cIMM3>
F;266-573/Domain: immunoglobulin homology cIMM5>
F;608-657/Domain: immunoglobulin homology cIMM5>
F;608-657/Domain: carboxyl-terminal propeptide #status predicted cCTP>
F;679-702/Domain: carboxyl-terminal propeptide #status predicted carboxyl end (Gly) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: JC1509
R; McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
R; McCuaig, X.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
A; Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopre
A; Reference number: JC1505; MUID:93273228; PMID:8500759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:Q61351; GB:X67280; Comment: This protein is expressed at the cell surface and plays a determinant role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
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F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;16-219/Domain: immunoglobulin homology <IMM1>
F;264-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;387,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEE 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW-----SP---LGEEGNV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 PELPKPSISSNNSKPVEDKDAVAFTC--EPETQDATYLWWVNNQSLPVSPRLQLSNGNRT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
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C;Species: Mus musculus (house mouse)
C;Date: 24-Feb_1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVNIQEPRQVKII------AW-----TSKTSVAYV----TPGDSETAPVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTLFNVTRNDTASYKCETONPVSARRSDSV 229
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Best Local Similarity 24.3%;
Matches 51; Conservative
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A,Molecule type: mRNA
A,Residues: 1-458 «MCC>
A,Cross-references: UNIPR
C,Comment: This protein i
C,Genetics:
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nonspecific cross-reacting antigen precursor - human
NyAlternate names: NCA; TEX/NCA
C;Species: Homo sapiens (man)
C;Dates: Homo sapiens (man)
C;Dates: J-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C;Accession: A26902; A29875; Ā27681; B31037; A29918; A27709; A36271; C26414; E44476; F47
C;Accession: A26902; A29875; A7781; B31037; A29918; A27709; A36271; C26414; E44476; F47
B;Otkawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys Res. Commun. 146, 464-469, 1987
A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) generate number: A26902; MUID:87298464; PMID:3619891
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A; Accession: A28875
A; Accession: A28875
A; Accession: A28875
A; Accession: A28875
A; Accession: A28875
A; Accession: A28875
A; Cross-references: Commun. 150, 89-96, 1987
A; Cross-references: Commun. 150, 89-96, 1987
A; Accession: A28875
A; Cross-references: CB: MID: 87204248; PMID: 3033672
A; Accession: A28875
A; Cross-references: CB: MID: 87204248; PMID: 3033672
A; Accession: A28875
A; Cross-references: CB: MID: 87204248; PMID: 3033672
A; Cross-references: CB: MID: 88106638; PMID: 3337731
A; Accession: A27681; MUID: 88106638; PMID: 3337731
A; Accession: A27681
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A; Residues: 1.238; V'.240-344 <TAW>
A; Reference number: A31037; MUID:89122014; PMID:3220478
A; Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and A; Reference number: A31037; MUID:89122014; PMID:3220478
A; Reference number: A31037
A; Residues: 1-137, L'.139-344 <BAR>
A; Residues: 1-137, L'.139-344 <BAR>
A; Residues: 1-137, L'. 139-344 <BAR>
A; Residues: L'AT, L'. 139-344 <BAR>
A; Cross-references: GB:M29541; NID:9189103; PIDN:AA59915.1; PID:9189104
A; Cross-references: GB:M29541; NID:9189103; PIDN:AA59915.1; Riggs, A.D.; Shively, J.E.
B; Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J; Biol. Chem. 263, 3202-3207, 1988
A; Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NA A; Accession: A29918; MUID:88139389; PMID:2830274
A; Accession: A29918
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A,Residues: 1-34 ARD:
A,Residues: 1-34 ARD:
A,Cross-references: GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
R,Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
B,cchem. Biophys. Res. Commun. 153, 1105-1115, 1988
A,Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and in.
A,Reference number: A27709; MUID:8826882; PMID:3390172
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A; Repidues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-23
R; Hefte, S.A.; Paxton, R.J.; Shively, J.E.
J. Blool. Chem. 265, 8618-8626, 1990
A; Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspec
A; Reference number: A36271; MUID:90256782; PMID:2341397
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A; Residues: 35-42; 44-53; 55-80; 83-134; 139-160; 166-172; 174-180; 191-194, 204-224; 233-308; 31
R; Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A; Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A; Reference number: A26414; MUID:87147209; PMID:3469650
EGN-VLOIFOTPEDQELTYTCTAQNPVS-NNSDSIS 186
                                                                A; Accession: A27709
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C; Keywords: brain, glycoprotein; membrane protein; phosphoprotein
F;1-7/Domain: signal sequence #status predicted <SIG>
F;1-3/As Region: hydrophobic
F;40, 66,136,148,279,287,300,315/Binding site: carbohydrate (Asn) (covalent) #status pred
F;42,115,142,164,171,220,231/Binding site: phosphate (Thr) (covalent) #status predicted
F;95,192,204,236,310/Binding site: phosphate (Ser) (covalent) #status predicted
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C;Species: Homo sapiens (man)
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Best Local Similarity
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A,Map position: 19913.2-19913.2
A,Map position: 22/1
A,Introns: 22/1
B,Introns: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            limbic-system-associated membrane protein precursor - human (Species: Howe sapiens (man) (Species: Howe sapiens (man) (Species: Howe sapiens (man) (Species: Howe sapiens (man) (Species: Howe) (Species: Howe sapiens (man) (Species: Howe sapiens) (
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A;Gene: lamp
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
                                                                                                                                                                                                                         estimation|of the size of the carcinoemb
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            A; Residues: 35-69 cPAX>
R; Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S. Genomics 14, 384-390, 1992
A; Title: Identification of three new genes and estimation of the size of the carcinoemth A; Reference number: A44476; MUID:93052339; PMID:1427854
A; Accession: E44476
A; Accession: E44476
A; Residues: 35-141 cKHA>
A; Residues: 35-141 cKHA>
A; Actual: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 35-141 cKHA>
A; Residues: 35-137, L', 139-141 cKH2>
C; Comment: This protein appears to be processed at the carboxyl terminus and anchored to contain the contain appears to be processed at the carboxyl terminus and anchored to contain the contain appears to be processed at the carboxyl terminus and anchored to contain the carboxyl terminus and cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
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12.7%; Score 131.5; DB 2;
Best Local Similarity 25.1%; Pred. No. 0.0015;
Matches 54; Conservative 29; Mismatches 67;
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Diliary glycoprotein h precursor - human (5pecies: Homo sapiens (man) (5pecies: Homo sapiens (man) (5pecies: Homo sapiens (man) (5pecies: Homo sapiens (man) (5pace: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004 (5Accession: JH0395 (F. Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y. R; Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y. A; Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y. A; Kitle: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones from the second 
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A/Residues: 1-31 «KUR»
A/Residues: 1-31 «KUR»
A/Residues: 1-31 «KUR»
A/Cross-references: UNIPROT:P13689, GB:M69176; NID:g179434; PIDN:AAA51825.1; PID:g179435.
A/Cross-references: UNIPROT:P13689, GB:M69176; NID:g179434; PIDN:AAA51825.1; PID:g179435.
A/Experimental source: leukocyte
C/Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C/Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-termin
F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEAN>
F/35-321/Product: biliary glycoprotein h #status predicted cAIG>
F/35-321/Product: biliary glycoprotein h #status predicted cAIC>
F/35-321/Domain: immunoglobulin homology cIMM1>
F/252-301/Domain: immunoglobulin homology cIMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 NTQADPYTTTKRYNLQIYRRLGKPKITQ-SLMASVNSTCNVTLTCSVE-KEEKNVTY-NW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 QIQHEPKTSQVYLIVQV-----PPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHL 168
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                                                                                                                                                                                                                                                                    31 IAWISKISVAYVIPGDSETAPVVIVIHRNYYERIHALGPNYNLVISDLRMEDAGDYKADI
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ch 12.0%; Score 125; DB 2; Length 338; I Similarity 27.4%; Pred. No. 0.0053; 43; Conservative 27; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTGREFEGEESYLEILGITREQSGKYECKAANEVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : : | | | | | | | : : RTLTLLSVTRNDTGPYECEIQNPVSANRSDPVT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 NVLQIFQTPEDQELTYTCTAQNPVS-NNSDSIS 186
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transmembrane carcinoembryonic antigen 3 precursor - human
NyAlternate names: CD66 splice form BGPc
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: C30127; 152597
R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; F,Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; F,Barnett, T.R.; Kretschmer, Austenative splicing accounts for the multiple mRNA
A;Fitle: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNA
A;Reference number: A92752; MUID:89139550; PMID:2537311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-464 cBAR.
A; Cross-references: UNIPROT: Q16170; EMBL: X16356; EMBL: X14784
A; Cross-references: UNIPROT: Q16170; EMBL: X16356; EMBL: X14784
B; Matt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Gschmeissner, S.E.; Hajibaghe:
Blood 84, 200-210, 1994
A; Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, exp.
A; Reference number: 152597; MUID: 94289702; PMID: 8018919
A; Accession: 122597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --KAD-INTQADPYTTTKRYNLQ 106
                                                                                                                                          -SP---LGEEG 154
                                                                                                                                                                                SMPFNVAEGKEVLLLYHNLPQQLFGYSWYKGERVDGNRQIVGYAIGTQQATPGPANSG-- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 VTVTHRNYYERIHALGPNYNLVISDLRMEDAGDY----KAD-INTQADPYTTTKRYNLQ
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                                                                                                                                              107 IYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW----
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                                                                                                                                                                                                                                                                  155 NVLOIFQTPEDQELTYTCTAQNPVS-NNSDSIS 186
                               VTVTHRNYYERIHALGPNYNLVISDLRMEDAGDY --
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Best Local Similarity
Matches 52; Conserv
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                         Circlesion: J40396
Rikuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem: Biophys. Res. Commun. 176, 578-58; 1991
A; Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A; Reference number: J40394; MUD:9122218; PMID:2025273
A; Reference number: J40394; MUD:9122218; PMID:2025273
A; Residues: 1-351 «KUR»
A; Residues: 1-351 «KUR»
A; Residues: 1-351 «KUR»
A; Residues: 1-351 «KUR»
A; Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C; Comment: Biliary glycoprotein; transmembrane protein
C; Superfamily: carcinoembryonic antigen precursor amino-termin C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
C; Keywords: glycoprotein; transmembrane protein
F; 1-134 Domain: carcinoembryonic antigen precursor amino-terminal homology «CEAN»
F; 1-34 Domain: signal sequence # status predicted «SIG»
F; 1-35 (Domain: immunoglobulin homology «IMM1»
F; 252-301/Domain: immunoglobulin homology «IMM2»
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A;Title: Three novel molecular forms of blitary glycoprotein deduced from cDNA clones fx A;Reference number: JH0394; MUID:91222218; PMID:2025273
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A;Residues: 1-417 <KUR>
A;Cross-references: UNIPROT:P13688; GB:M72238; NID:g179436; PIDN:AAA58394.1; PID:g179438
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Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
's Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
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'1-34/Domain: signal sequence #status predicted <SIG>
'1-34/Domain: signal sequence #status predicted <MAT>
'155-31/Domain: immunoglobulin homology <IMM1>
'156-21/Domain: immunoglobulin homology <IMM2>
'131-398/Domain: immunoglobulin homology <IMM2>
'131-398/Domain: immunoglobulin homology <IMM3>
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C,Species: Homo sapiens (man)
C,Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
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Matches 52; Conserv
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Run on:

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MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
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rattus norv
homo sapien
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mus musculu
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                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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009et39
008nd32
006wg1
00cz17
00cz17
00cp2j4
00sp39
009ng26
009ng26
003291
0040cg3
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Palou E., Gold J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, FAFO4817; AAF21723.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-11ke.
SMART; SM00409; IG; 1.
PROSITE; PS05155; IG LIKE; 1.
SEQUENCE 272 AA; 30514 MW; GAZE13AA4E22E13E CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD84d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 199; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                  272 AA
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06UWG1
06UWG1
06ZXI7
06EZ4-
06EZ4-
06EZ4-
06EZ4-
09ND2-
09ND2-
09NO2-
SLAM HUMAN
096QR3
064 0R3
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095660,
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01-OCT-2003 (TrEMBLre)
CD84,
HOMO SAPIEDS
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
  Name=CD84;
   239
180
177.5
172.5
172.5
165.5
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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LY9 HUMAN
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Q91XA0
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Q8BHK6
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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A STEADLE-Lymph,

X. MEDINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X. TISSUE-Lymph,

X. Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

X. Attaschul S.F., Zeeberg B.S., Wagner L., Shenmen C.M., Schuler G.D.,

Attschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Ehat N.K.,

A Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

X. Balatchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L.,

X. Bapleton M., Soares M.B., Bonaldo M.F., Caranori F.D., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X. Hilaton D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

X. Halton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Tonniski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Tonnes S.J., Marra M.A.,

R. Tonnes S.J., Marra M.B.,

R. Tonnes S.J., 
                                                         MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                                                                                             01-73A-1998 (TrEMBLrel. 05, Created)
01-73A-1998 (TrEMBLrel. 05, Last sequence update)
25-077-2004 (TrEMBLrel. 28, Last annotation update)
Leukocyte antigen CD84 (Leukocyte differentiation antigen CD84 isoform CD84)__(MAX.3 cell surface antigen precursor) (CD84 antigen).
                                                                                   MEDITNE-86188202; PubMed=3008886; Anteresen R. Bross K.J., Osterholz J., Emmrich F.; Horss K.J., Osterholz J., Emmrich F.; Human macrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation antigens."; Blood 67:1257-1264(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazona,
Wammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97454416; PubMed=9310491;
de la Frente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
"CD84 leukocyte antigen is a new member of the Ig superfamily.";
Blood 90:2398-2405(1997).
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Palou B., Freed J.H., Sole J., Pi A., Vilella A., Vives J., Gaya A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U96627, AAD04232.1, -.
InterPro; IPR003599; Ig.
InterPro; IPR07110; Ig-like.
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bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
Korn B., Zuo D., Hu Y., LaBaer J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR541847, CAG46645.1;
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig.
SMART; SM00409; IG; 2.
PROSITE; PSS0835; IG_LIKE; 1.
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PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 280 AA; 31651 MW; A043E048E762A718 CRC64;
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ive 0; Mismatches 0;
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Pred. No. 1.9e-82;
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05-JUL-2004 (TrEMBLrel. 27,
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Name=CD84;
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61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 120
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 1039; DB 2; Length
Best Local Similarity 100.0%; Pred. No. 2e-82;
Matches 199; Conservative 0; Mismatches 0; Indels
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054816; AAF21722.1; -.
Genew; HGNC:1704, CD84.
InterPro; IPR003599; Ig.
InterPro; IRR007110; Ig-like.
SMART; SM00409; IG; 1.
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SEQUENCE 345 AA; 38782 MW; DAO6BC5A682E62DE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD84a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte antigen CD84 (Fragment).
                                                                                                                                                                                                                                                                                                                                                     345 AA
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                                                                                                                                                                                                                                      202 NSDSISARQLCADIAMGFR 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=CD84;
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              61
                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OlymAR. 2002 (TrEMBLrel. 20, Created)
01-MAR. 2002 (TrEMBLrel. 20, Last sequence update)
01-ORT-2003 (TrEMBLrel. 25, Last annocation update)
Leukocyte differentiation antigen CD84 precursor.
Homo saptens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 328;
                                                        A Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; 1020981; AAR91341.1;
R EMBL; A7223124; AAR71721.1;
R EMBL; AJ2231324; CAA11264.1;
R EMBL; AJ2231324; CAA11264.1;
R EMBL; BC020063; AAR20063.1;
R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0005987; C:integral to plasma membrane; TAS.
R GO; GO:0007156; P:homophilic cell adhesion; TAS.
R InterPro; IPR005199; IG.
R InterPro; IPR007110; Ig-like.
R SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAX.3 cell surface antigen.; 6C9A89206A6D0344 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1039; DB 2;
100.0%; Pred. No. 1.9e-82;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 AA
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22 328 MA
328 AA; 36871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0
Matches 199; Conservative
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Matches 199; Conservative
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                  SEQUENCE FROM N.A.
TISSUE=Lymph;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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QBWWIB;
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SIGNAL
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142 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 201
    82 YERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 KGRIEIIDQKYDLVIRDLRWEDAGTYKADINEENEE-TITKIYYLHIYRRLKTPKITQSL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN 180
                                 MASVNSTCNVTLTCSVEKEEKNVTYNWSPLGEEGNVLQIFQTPEDQELTYTCTAQNPVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                        Engel P.;
"Molecular cloning, characterization, and chromosomal localization of the mouse homologue of CD84, a member of the CD2 family of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 KDADPUVMNGILGESVTFLLNIQEPKKIDNIAWTSQSSVAFIKPGVNKAE--VTITQGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                                                                                                       Name=cd84; Synonyms=cD84;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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Q9HBGT; Q14775; Q9HAN5; Q9NQ24;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen (Cell-surface molecule Ly-9) (CD229 antigen).
Name=LY9;
                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Peritoneum;
MEDLINE=99180614; PubMed=10079287; DOI=10.1007/8002510050490;
de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 329;
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Immunogenetics 49:249-255(1999).
EMBL, AP043445, AAD02273.1;
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
SMART; SM00409; IG LIKE; I.
SROUNDER 329 AA; 37345 MW; 43BBIAASAF1989E0 CRC64;
                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                     329 AA
                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                     PRT;
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                                                                                             181 NSDSISAROLCA 192
                                                                                                                         NSDSISAROLCA 213
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                                                                                                                                                                                                                                                                          CD84 leukocyte antigen
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Q9Z178;
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ID LY9 H

AC 09HBG

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DT 28-FE

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       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                         Length 197;
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96.5%; Score 1003; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.8e-79;
Matches 192; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palou E., Sole J., Pirotto F., Gaya A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF054818; AAF21724-1; -.
InterPro; IPR003599; IG.
InterPro; IPR07110; Ig-like.
SMART; SM00409; IG, 1.
EROSITE; PSS0815; IG LIKE; 1.
SEQUENCE 241 AA; Z6902 MW; F0121BC1609B6C52 CRC64;
                                                                                                                                                                                                                         NON_TER 197 197
SEQÜENCE 197 AA; 21889 MW; 2E660BF5FAB71D88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JG_LIKB, 1.
; Z6902 MW; F0121BC1609B6C52 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Leukocyte differentiation antigen CD84 isoform CD84s.
                                                                                                                                                                                                                                                                      96.5%; Score 1003; DB 2; llarity 100.0%; Pred. No. 1.4e-79; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AA
                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity
Matches 192; Conserv
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TISSUE=Pooled tissue;
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                                                                                                                                                                                                                                          602 6
655 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                        McKenzie I.F.; "and characterization of cDNA clones for Humly9: the human "Isolation and characterization of cDNA clones for Humly9: the human lumunogene of mouse Ly9."; Immunogenetics 43:13-19(1996).
                                                                                                                                                                                                                                                     ZBQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A., Margolin J.F.;
Margolin J.F.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May participate in adhesion reactions between T lymphocytes and accessory cells by homophilic interaction.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 600684; -.
GO; GO:0005887; C:integral to plasma membrane; ISS.
GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.
                                                   SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
Gene structure of the mouse leukocyte cell surface molecule Ly9.";
Immunogenetics 51:788-793(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                Isold=Q9HBG7-3; Sequence=VSP 002524, VSP 002525, VSP 002526; SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking for some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-lymphocyte surface antigen Ly-9.
Extracellular (Potential).
Potential.
                                                                                                                                             Sandrin M.S., Henning M.M., Lo M.F., Baker B., Sutherland G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
19-like V-type 1.
19-like C2-type 1.
                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q9HBG7-2; Sequence=VSP_002525;
                                                                                                                       SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2). MEDLINE=96128248; PubMed=8537117;
                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9HBG7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF244129; AAG14995.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, L42621; AAA92623.1; -. EMBL, AL121985; CACO0580.1; -. EMBL, AY007142; AGG02002.1; -. Genew, HGNC:6730; LY9.
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InterPro, IPR007110; Ig-like.
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    sapiens (Human)
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48 KDSAPTVVSGILGGSVTLPLNISVDTEIENVIWIGPKNALAFARPKEN-----VTIMVKS 102
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
33.9%; Score 352; DB 1; Length 655;
Best Local Similarity 38.1%; Pred. No. 4.4e-22;
Matches 77; Conservative 41; Mismatches 70; Indels
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N-linked (GlCNAc...) (N-linked (GLCNAc...) (M-linked (G
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28, Last annotation update)
(SLAM family member 9).
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Missing (in Ref. 1).
V -> M (in Ref. 4).
Ig-like C2-type 2. Potential.
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SEQUENCE FROM N.A.
TISSUE=B lymphocyte;
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68 GPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNST 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | | | : | | : | : | : | 30 VVAVLQESISLPLEIPPDEEVENIIMSSHKSLATVVPGKEGHPATIMVTNPHYQGQVSFL
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pooled tissue;
Director MGC Project;
Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275725; AAK69052.1; -.
EMBL; AF034613; AAK61395.1; -.
EMBL; BC074754; AAH47154.1; -.
Genew; HGNC:18430; SLAMF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jenew, HGNC:1843v; IG.
InterPro: IPR003599; IG.
InterPro: IPR003109; IG.
SMART; SMO0409; IG; IG.
PROSITE; PS50835; IG LIKE; I.
PROSITE; PS50835; IG LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.0%; Score 332; DB 2; 38.1%; Pred. No. 8.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%; Preα. ....
ive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 38.1% tes 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TremBirel.
01-MAR-2004 (TremBirel.
SLAM family member 9.
Name=Slamf9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $ 210
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
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Matches
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B. Buenow K.H., Schaefer C.F., Bhat N.K.,
RA S.J., Wordan H., Moore T., Max S.I., Wang J., Hong L.,
Rab S.S., Loquellano N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rohas S.S., McKennan K.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabesley S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rohiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rohiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rohiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ASVNSTCNVTLTCSVEKEEKNVTYNW-----SPLGEEGNVLQIFQTPEDQELTYTCTAQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 DEDPBEVIGVLOESINLSLEIPSNEEIKHIDWLPQNNIAIVKPGKKGQPAVITAVDPRYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 DSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amotation update)
Mus musculus B lymphocyte B cells CRL-1702 WEHI 231 cDNA, RIKEN full-
length enriched library, clone:G430073H03 product:weakly similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.6%; Score 328.5; DB 2; Length 285; 36.7%; Pred. No. 1.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stransberg R.,
Stransberg R.,
Stransberg R.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019477; AH19477.1; -.
MGD; MGI:1923692; Slamf9.
GQ; GQ:0005615; C:extracellular space; TAS.
GQ; GQ:0005615; C:extracellular space; TAS.
SWART; SW00409; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 285 AA; 31728 MW; D84BFF8142367F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=FVB/N; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 NPVSN-NSDSISARQLCAD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
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Best Local Similarity
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122 ASVNSTCNVTLICSVEKEEKNVTYNW-----SPLGEEGNVLQIFQIPEDQELTYTCTAQ 175 ERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTIKRYNLQIYRRLGKPKITQSLM 121

DEDPEEVIGVLQESINLSLEIPSNEEIKHIDWLFQNNIAIVKPGKKGQPAVIMAVDPRYR 81

62

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193

NPVSN-NSDSISARQLCAD

176 202

||||| :| || || NPVSNISSHRISVGSFCAD 220

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TISSUB-B lymphocyte;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-B. Lymphocyte;

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nahai K., Nahasa T., Mishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sahraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Toya T., Toya T., Yawunishi A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=B lymphocyte;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=B lymphocyte;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                       RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.1%; Score 323.5; DB 2; Length 285; 36.2%; Pred. No. 4.8e-20; ive 31; Mismatches 89; Indels 7.
                                                                                                                                                 MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48675E0611027B3B CRC64;
                   Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0016021; C:extracellular space; TAS. GO:0016021; C:integral to membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50835; IG LIKE; 1.
285 AA; 31759 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK090041; BAC41061.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                      Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:1923692; Slamf9
                                                                                                                                 TISSUE=B lymphocyte;
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                                                                                                              SEQUENCE FROM N.A
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The FANTOM Consortium, Lthe RIKEN Genome Exploration Research Group Phase I & II Team; Lthe RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUB=Tongue;
MEDLINE=20499374; PubMed=110421S9; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J; TISSUE-Tongue;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/63; TISSUB=Tongue;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Milbata K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishine T., Tashiro H., Itch M., Sumanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
STRAIN=C57BL/6J; PubMed=11217851; DOI=10.1038/35055500;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                      enriched
14-H1 (CD2
                                                                                                                                                           CD84-H1
                                                                       01-JTN-2001 (TrEMBLrel. 17, Created)
01-JTN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue CDNA, RIKEN full-length (library, clone:2310026104 product:weakly similar to CD8
                                                                                                                                                                                                                                                                                                                                                                                    Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                    285 AA.
                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                         Name=Slamf9;
                                                                                                                                                                library, cl
FAMILY 10)
                                                        0907060;
                                         090780
                                                                                                                                                                                     FAMILY
RESULT 14
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5 61

Gaps

7;

Best Local Similarity 36.2 Matches 72; Conservative

Query Match

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Exp. Med. 194:235-246(2001).
                                                       ERRATUM.
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         SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB=Tongue;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Rato H.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Nishi K., Nomura K., Numazaki R., Ohno M.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Sakai C., Sakai C., Saito H., Sano H., Sasaki D., Shibata K., Shibata Y., Shibata T., Shibata K., Shibata K., Shibata K., Shibata K., Shibata K., Shibata K., Shibata T., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Murametsu M., Hayashizaki Y., Yasunishi A., Yoshida K., Yoshino M.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
REL: AKOOSSOS: Babe 2528.1;
Shibata Shamfs.
GO; GO:0016021; C:integral to membrane; TAS.
RINterPro; IPR007110; Ig-like.
RERET: MADA 1991; Ig-like.
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Q96DU3; Q96DV0;

Q5-JUL-2004 (Rel. 44, Last sequence update)

S5-JAN-2005 (Rel. 46, Last annotation update)

SLAM family member 6 precursor (NK-T-B-antigen) (NTB-A) (Activating NK receptor) (UNG6123/PRO20080).

Name=SLAMF6; Synonyms-KALI;

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., FUNCTION, PHOSPHORYLATION, TISSUE SPECIFICITY, AND INTERACTION WITH SH2DIA/SAP; PIN6 AND PIN11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "NTB-A, a novel SH2D1A-associated surface molecule contributing to the inability of natural killer cells to kill Epstein-Barr virus-infected B cells in X-linked Lymphoproliferative disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=21382389; PubMed=11489943;
Bottino C., Falco M., Parolini S., Marcenaro E., Augugliaro R., Sivori S., Landi E., Biassoni R., Notarangelo L.D., Moretta L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 285;
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 285 AA; 31764 MW; 33BDB4A633ASC1B3 CRC64;
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                                                                                                                    MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Mend J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Raton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., A Huang A., Xim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Sashagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Andlen R., Wasanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;
The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pubmed=1540161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally
verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
-!- FUNCTION: Triggers cytolytic activity only in natural killer cells
(NK) expressing high surface densities of natural cytotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: Interacts with PTN6 and, upon phosphorylation, with PTN11 and SH2DIA/SAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Expressed by all (resting and activated) natural Killer cells (NK), T and B lymphocytes.
-!- PTM: Phosphorylated.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 1.
PROSITE; PS50815; Ig LiKE; 1.
Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
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(Potential).
(Potential).
(Potential).
(Potential).
Bottino C., Falco M., Parolini S., Marcenaro E., Augugliaro R.,
Sivori S., Landi E., Biassoni R., Notarangelo L.D., Moretta L.,
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Potential.
Cytoplasmic (Potential).
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By similarity.

N-linked (GlcNAc.)

                                                                         Exp. Med. 194:705-705(2001).
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H-InvDB; HIX0019182; ..
MIM; 606446; ..
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                                                                                  Query Match 30.5%; Score 316.5; DB 1; Length 332;
Best Local Similarity 36.9%; Pred. No. 2.4e-19;
Matches 73; Conservative 43; Mismatches 69; Indels 13; Gaps
266 266 Missing (in Ref. 1, CAC59749).
332 AA; 37345 MW; 46D8141A0D198091 CRC64;
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Search completed: February 4, 2005, 12:15:01 Job time : 88.4394 secs

(otqsu) Anolg @Qoq siri;

Adi22889 CDNA erco Adh73891 Human sec Adh23942 PRO polyp Aai72383 CD84 codi Adq23399 Human sof Acq23399 Human bre Aal24045 Human bre Aax41382 Human sec

Sequence:

Run on:

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Searched:

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Human; immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carcinoma, autoimmune disorder; multiple sclerosis; Grave's disease; Hashimoto's disease; acquired immune deficiency syndrome; hepatotropic; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psociasis; apoptoric disorder; systemic lupus erythematosus; bronchitis; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; damonphilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; antinflammatory; Crohn's disease; osteopathic; antibacterial; immunomodulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AIDS; CD84; gene; de.
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/product= "Human CD84 protein"
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                                                                                                                    ACN92105
AAL24045
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ADK98595
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ABK69998
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ADC57102
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ADC3340
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   Command line parameters:
-MODEL=frame+ p2n.model-DEV=xlh
-Q=/Cqn2_1/USPTO gpool/USO9882171/runat_04022005_I144003_26015/app_query.fasta_1.910
-Q=/Cqn2_1/USPTO gpool/USO9882171/runat_04022005_I144003_26015/app_query.fasta_1.910
-Q=/Cqn2_1/USPTO gpool/USO9882171/runat_BUFFIX=rsng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UMITS=bits -STRAT=1 -ENN=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODEL-CAL.-OUTFWT=pto -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MALIGN=15
-NORMAP -LARGEQUERY -NGG GCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -LONGLOG
-FGAPOP=10 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                           nucleic search, using frame_plus_p2n model
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Database

Result Š

Adb99815 Human PRO Adb99470 Novel hum

Adk988595 Human imm
Abs76363 DNA encod
Ada187104 Human NOV
Ad187102 Human NOV
Ad0571102 Human NOV
Ad078173 Human LyAd4078173 Human LyAd4078173 Human LyAd407817 Human CD2
Abv77939 Hypoxia-i
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Abx08617 CDNA encod
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| MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGluAlaAspProTyrThr 120
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ThriysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human leukocyte differentiation antigen CD84 encoding DNA.
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Immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple sclenosis, Grave's disease, and Hashimoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (1g)), inflammatory bowel disease (e.g. rheumatoid arthritis and osteoarthritis), allergic inflammatory disorders (e.g. rheumatoid asthritis and osteoarthritis), allergic inflammatory disorders (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, chronic obstructive pulmonary disease (e.g. emphysema), bronchitis, carhesis, cachesia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, acute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is useful in screening assays, pronosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. human CD84 DNA
                                                                                                                                                                                                                                                                                                                         Novel isolated polypeptide containing immunoglobulin and immunoglobulin-
like domains and SLAM associated protein, termed CD2000 or CD2001, useful
for treating immune, inflammatory, or hepatic circulatory disorders.
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                                                                                                    02-NOV-2001; 2001EP-00309339
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                                                                                                                                          03-NOV-2000; 2000US-00706167
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Best Local Similarity:
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                             MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
                                                                                                               LeuMet AlaSerVal AsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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benefits from modulating the balance of regulatory T cell function
catalive to effector T cell function, or vice versa, in a subject. The
method involves administering an agent that modulates the expression or
activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1,
CRP-32, CD83, cD84, CD89, serotonin R2C, GBR63,
CHSTARIAN RAC, GBR58, EPD-R, PSG-1, PSG-3, PSG-9, PDE-4d, and PI-
3-related kinase to the subject, such that treatment occurs. The methods
care useful for diagnosing, preventing or treating conditions
characterized by a too-vigorous or weak effector T cell or regulatory T
cell response to antigens associated with the condition, such as in an
allergic response, an autoimmune disorder, a viral infection, a microbial
infection, a parasitic infection or a tumour. The present sequence
represents a DNA encoding a human leukocyte differentiation CD84 antigen,
preferentially expressed in regulatory T cells.
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                                                                                                                                                                                                                                                                                                                        Treating a condition that benefits from modulating regulatory or effector T cell function comprises administering an agent that modulates the expression or activity of a gene or polypeptide (e.g. PIGER2, IGFbetal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
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                                                                                   09-OCT-2002; 2002US-0417102P.
09-OCT-2002; 2002US-0417103P.
09-OCT-2002; 2002US-0417243P.
18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424777P.
08-NOV-2002; 2002US-0424777P.
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                                                                                                                                                       invention relates to a novel method for detecting soft tissue sarcoma
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                                                                                                                                                               which comprises obtaining a first soft tissue sample from an individual determining the first soft tissue sample from a normal soft tissue sample from an individual determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sample indicates the presence of soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the
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                                                                    Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                     specification per se but was submitted in CD format by the inventor.
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(PROT-) PROTEIN DESIGN LABS INC
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GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGGTAATGTCCTTCAAATC
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Greene JM;
                                                                                                                                                              Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                                                                                               Claim 1; Page 402-404; 721pp; English.
      970S-0056889P
970S-0056892P
970S-0056893P
970S-0056903P
970S-0056908P
970S-0056908P
970S-0056910P
970S-0056911P
970S-0057669P
970S-0057669P
970S-0057669P
                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                              WPI; 1998-506364/43.
P-PSDB; AAW74891.
                                  22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                             22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
05-SEP-1997;
                                                                                                  05-SEP-1997;
05-SEP-1997;
12-SEP-1997;
02-OCT-1997;
                 22-AUG-1997;
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This sequence represents a nucleic acid molecule designated Gene 164 from the human cDNA clone HSAMF26 (deposited as clone ATCC 97903 and ATCC 209049) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin C protein as compared to the human protein only. The invention relates to protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-059912; amino acid sequences AAW74731-WY5056) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polynucleotides.

Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses)

Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB: US-09-882-171-483 (1-3 Qy 1 MetAlaGl Qy	res: arity: milarity: -483 (1-32	Alignment Scores: Pred. No.: 1695.00 Scores: Scoret Similarity: 100.00\$ Mismat Query Match: 2 100.00\$ Mismat Conservery Match: 2 100.00\$ Mismat Conservery Match: 2 100.00\$ Mismat Conservery Mismat Conservery Match: 39.94\$ Mismat Conservery Mismat Conservery Match: 2 100.00\$ Mismat Conservery Mismat Conservery Mismat Conservery Mismat Conservery Mismat Conservery Mismat Conservery Mismatch Mismatch Conservery Mismatch Cons	Length: Matches: Conservative: Mismatches: Indels: Gaps: 1-3173) LeuLeuLeuCysLeu(ores: 2.27e-163 Length: 3173 1695.00 Marches: 328 larity: 100.00\$ Conservative: 0 imilarity: 100.00\$ Mismarches: 0 imilarity: 100.00\$ Mismarches: 0 2 Indels: 0 Gaps: 0 1-483 (1-329) x AAV59674 (1-3173)	20
Db 51	ATGGCTCAG	CACCACCTATGGATC	TTGCTCCTTTGCCTG	51 ATGGCTCAGCACCCATGGATCTTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGCT 111	7 5
ογ 21	GlyLysAsp	SerGluIlePheThrValAsnGly	ValAsnGlylleLeu 	21 GlyLysaAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSeFYAIlIRFNEFFO 40	4 6
	GGAAAAGAC	TCAGAAATCTTCACA	GTGAATGGGATTCTG	111 GGAAAAGACTCAGAAATCTTCACAGTGAATGGGATTCTGGGAGAGTCAGTC	1
Ωγ 41	ValAsnile	GlnGluProArgGln 	ValLysileileAla' 	41 ValAsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerVal 60	9
Db 171	GTANATATO	CAAGAACCACGGCAA	GTTAAAATCATTGCT	171 GTAAATATCCAAGAACCACGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTT 23	23

61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80

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970S-0038621P.
970S-0040161P.
970S-0040161P.
970S-0040163P.
970S-0040333P.
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970S-0043578P.
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             Homo sapiens
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231 GCTTATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAAT 290
                                                                                                                                                                                                   GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver meoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorders; Alzheimer's disease; infection; cocular disorder; cerebral infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
                                                                                                                                                                                                                                          PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer
                                                                                                                                                                                                                                                                                                                                        TyrTyrGluhrg1leHisAlaLeuGlybroAsnTyrAsnLeuVal11eSerAspLeuArg
                                             291 TATTATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGG
                                                                         MetGluaspalaglyasptyrLysalaaspIleasnThrGlnalaaspProTyrThrThr
                                                                                                                  ThrLysArgTyrAsnLeuGln1leTyrArgArgLeuGlyLysProLys1leThrGlnSer
                                                                                                                               411 ACCAAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGT
                                                                                                                                                          LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
                                                                                                                                                                       GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                             261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a sequences also given in the specification. The protein is used in a can pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, by pacteria, viruees and fungi and ocular disorders infections. The polypeptides can also be used to aid wound can maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The prepared as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, coffactors and other nutritional components. The present sequence represents a cDNA derived from a gene Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or Example 1; SEQ ID NO 174; 129pp; English.

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970S-0047584P.
970S-0047585P.
970S-0047586P.
970S-0047588P.
970S-0047588P.
970S-0047589P.
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970S-0047612P-
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970S-0048974P-
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            97US-0047582P
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   Human, secreted protein, hyperproliferative disorder; leukaemia; breast cancer; wound; reproductive disorder; blood-related disorder; has breast cancer; wound; reproductive disorder; blood-related disorder; has been cancer; wound; reproductive disorder; multiple sclerosis; wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis; graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma; wiral infection; hinfection; fungal infection; AIDS; sepsis; went disorder; kidney failure; cardiovascular disorder; cytostatic; angina pectoris; cerebral ischaemia; congenital heart defect; angina pectoris; cerebral ischaemia; congenital heart defect; angina pectoris; neurological disorder; Alzheimer's disease; parkinson's disease; inflammation; Crohn's disease; vulnerary; memunosuppressive; antibacterial; haemostatic; thrombolytic; antianginal; antiasthmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal; cerebroprotective; cardiant; nootropic; antiparkinsonian; antiinflammatory; gene; ss.
                                                      GluIleLeuGlnSerLygValLeuProSerLysGluGluProValAsnThrValTyrSer 300
                                         GluValGlnPheAlaAspLvsMetGlvLvsAlaSerThrGlnAspSerLysProProGly 320
                                                                                                                                                                                                                CDNA sequence #164 containing coding region of a human secreted protein.
            ACD82804 standard; cDNA; 3173 BP
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97US-0040162P.
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Indels:

99.948

Query Match: DB:

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The present invention relates to the isolation or movel numbars becreated proteins and the polynucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polynucleotide sequences for the secreted proteins are useful for preventing, treating, ameliorating or diagnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive disorders (e.g. leukaemia or breast cancers), wounds, reproductive thymic hypoplasia), immunodéficiencies (e.g. hamophilité solerosis or Hashimoto's thyvoiditis), allesques (e.g. archma), rival or bacterial or fungal infections (e.g. Miskott-Aldrich syndrome or thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease, viral or bacterial or fungal infections (e.g. AlDS or sepsis), remplained alsorders (e.g. Alzhelmer's disease). The pectoris, cerebral ischaemia or congenital heart defects), respiratory disorders (e.g. Alzhelmer's disease). The polymucleotide or polypeptide may also be used as vaccine adjuvants.

ACDB2641-ACDB2950 encode human secreted proteins or their fragments. ACDB2641-ACDB2950 encode human secreted proteins or their fragments.

Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to the isolation of novel human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carter KC, Bednarik DP;
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08-SEP-1998; 98US-00149476
17-MAR-2000; 2000US-0190068P
                                                                                                                                                                                                YOUNG P E.
GREENE J M.
GREENE A M.
DUAN D R.
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FLORENCE K A.
OLSEN H S.
FISCHER C L.
BEBNER R.
BREWER L A.
MOORE P A.
SAIT Y.
LAPLEUR D W.
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ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-521800/49.
P-PSDB; ABO34537.
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KYAW H.
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FENG P.
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(ZENG/)
(KYAW/)
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(LAFL/)
                                                                                                                (BEDN/)
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                                                                                                                                                                                                   (YOUN/)
(GREE/)
                                                                                                                                                                                                                                                                    (FLOR/)
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                                                                                                                                                                                                                                                                                                                                                                            (MOOR/)
                                                                                                    CART/
                                                                                                                                                                                                                                     (PERR/)
(DUAN/)
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Ferrie AM;

Ebner R;

3173 328 0

Length: Matches: Conservative: Mismatches:

2.27e-163 1695.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

Alignment Scores:

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GAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGG 1010
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                                                                                                                  AlaryrvalThrProGlyAspSerGluThrAlaProvalValThrValThrHisArgAsn
                                                                                                                                                             ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer
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                                                            GlyLysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro
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                                                                                                        ValAsnileGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerVal
                    Met AlaGlnHisHisLeuTrpIleLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla
US-09-882-171-483 (1-329) x ACD82804 (1-3173)
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08-SEP-1998; 98US-00149476
17-MAR-2000; 2000US-0190068P
16-MAR-2001; 2001US-00809391
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NI J.
FENG P.
YOUNG P.
YOUNG P.
FERRIE J M.
FERRIE A M.
DUAN D R.
FLORENCE K A.
OLSEN H S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
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BREWER L A.
MOORE P A.
SHI Y.
LAFLEUR D W.
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
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(SHIY/)
(LAFL/)
   cytostatic; gene therapy; cancer; human; secreted protein; gene; ss.
                                                                                                                cDNA encoding novel human secreted protein seq id 174
                            ADI22889 standard; cDNA; 3173 BP.
                                                                                                                                                                                                                                                                                     97US-0038621P

97US-0040162P

97US-0040333P

97US-0040334P

97US-00403311P

97US-00433112P

97US-0043313P

97US-0043313P

97US-0043313P

97US-0043313P

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97US-004356P

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97US-004356P

97US-004358P

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97US-004358P

97US-004758P

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                                                                                    22-APR-2004 (first entry)
                                                                                                                                                                                                   US2003175858-A1
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                               18-SEP-2003
                                                         ADI22889;
            ADI 22 AD 12 RESULT 7
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                                                                                                                                                                                                                                        261 IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp
                                                                                                                                                                                                                                                                                              GlulleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer
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                                                                                                                                     651 AACAATTCTGACTCCATCTCTGCCCGGCAGCTCGTGCAGCATCGCAATGGGCTTCCGT
                                                                                                                                                                                 111 ACTCACCACACGGGTTGCTGAGCGTGCTGGCTGCTATCTTTCTGTCTCATTCTG
                                                                                                                                                                                                                        SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr
GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle
                                                     PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; secreted protein; cancer; haematopoietic disorder; endocrine disorder; immune system disease; inflammatory disorder; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 ThrSerSerTyrGluIleValile 328
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97US-0040161P.
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07-MAR-1997;
07-MAR-1997;
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
11-APR-1997;
11-APR-1997;
11-APR-1997;
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                                                                                                                                                                                                                                                    The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a polynpeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or amelicating a medical condition e.g., cancer. The sequence encodes a novel human secreted protein of the invention.
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                                                                           Ferrie AM;
                                                                                                                                                                         New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition
                                                            Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AN
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                  WPI; 2003-898535/82.
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Best Local Similarity:
                                                                                                                                                P-PSDB; ADI23198
       (ZENG/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
                                                                                                                                                                                                          e.g., cancer.
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970S-0047581P

970S-005661P

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PR 22-AMG-1997; 9705-00568919.
PR 22-AMG-1997; 9705-00568919.
PR 22-AMG-1997; 9705-00568919.
PR 22-AMG-1997; 9705-00568019.
PR 22-AMG-1997; 9705-0056919.
PR 22-AMG-1997; 9705-0057819.
PR 05-SEP-1997; 9705-0057819.
PR
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ValAsnileGlnGluProArgGlnValLySileIleAlaTrpThrSerLySThrSerVal

US-09-882-171-483 (1-329) x ADH73891 (1-3173)

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Length: Matches: Conservative: Mismatches:

2.27e-163 1695.00 100.00% 100.00% 99.94%

Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

Pred. No.:

Indels:

Gaps:

15-SEP-2003; 2003WO-US029097 16-SEP-2002; 2002US-0411392P

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25-MAR-2004

Homo sapiens.

(GETH) GENENTECH

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                 TyrTyrGluhrgileHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArg
                                                                                                                                         ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer
                                                                                                                                                                                  LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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GTAAATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTT
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The present invention relates to PRO proteins and their coding sequences. The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polyeaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, immunodeficiency with hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's Iymphoma, intermediate lymphoma, follicular lymphoma, type II hypersenstivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypodrenocorticism, glomerulonephritis, or anxionament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development
                                                                                                                                                                                                                                                                                                                     New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
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Wu TD;
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U; 0 Other; 3299 328 0 0 0 Length: Matches: Conservative: G; 791 T; 0 Mismatches: Indels: Gaps: 750 BP; 956 A; 802 C; 2.4e-163 1695.00 100.00% 100.00% 99.94% Similarity: Percent Similarity: Sequence 3299 Alignment Scores: Query Match DB: Best Local

(1-3299)US-09-882-171-483 (1-329) x ADL82906

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1 MetalaglnHisHisLeuTrplieLeuLeuLeuCysLeuGlnThrTrpProGluAlaAla 20
21 GlytysaspserGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro 40
105 GGAAAAGACTCAGAAATCTTCACAGTGAATGGGATTCTGGGAGAGTCAGTC
41 ValAsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60
GTAAATATCCAAGAACCACGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTT 224
61 AlaTyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 80
GCTTATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAAT 284
81 TyrTyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArg 100
285 TATTATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGG 344

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                                                                                                                                                                                                                                                                                                                                                               LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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               ATGGAAGACGCAGGAGCTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC
                                 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer
                                               ACCAAGGGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGT
                                                                              TTAATGGCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAGAA
                                                                                                       GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle
                                                                                                                 GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATC
                                                                                                                                          PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer
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The invention relates to a novel isolated nuclear and the Fro polypeptide encoded by it. A protein of the invention has antidatherity, and respiratory activity. A polymuclectide of the invention may have a use in gene therapy. The PRO polymelectide of the invention may have a use in gene therapy. The PRO polymelectide of the invention may have a use in gene therapy. The PRO polymelectide, its agonist, antagonist, or antibody that specifically binds to the colypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, invenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Slogren's syndrome, systemic chromic arthritis, diabetes mellitus, immune-mediated renal thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal chrome, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, dillain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, dillain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, whipple's inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, arthma, allergic rhinitis, atopic dermatitis, food disease, arthma, allergic rhinitis, atopic dermatitis, coddisease, arthma, allergic rhinitis, atopic dermatitis, coddisease, arthma, allergic rhinitis, atopic dermatitis, protein of centiophilic pneumonilis, an immunologic disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a novel isolated nucleic acid and the PRO
                                                                                                     Wood WI;
                                                                                                     Williams PM,
                                                                                                     Van Lookeren M,
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(GETH ) GENENTECH INC
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Wu TD;
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                                                                                                                                                                                              SerSerValPheLeuPheArgLeuPheLysArgArgGlnAspAlaAlaSerLysLysThr
                                                                                                                                                                                                                                                                                       IleTyrThrTyrIleMetAlaSerArgAsnThrGlnProAlaGluSerArgIleTyrAsp
                                                                                                                                                                                                                                                                                                GlulleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer
                                                                                                                                                                                                                                                                                                                                    GAAATCCTGCAGTCCAAGGTGCTTCCCTCCAAGGAAGAGCCAGTGAACACAGTTTATTCC
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                                                                                                                           PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer
                                                                                                                                                           AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg
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                                                                                              GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIle
                MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
                            ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer
                                                         405 ACCAAGGGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGGGT
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                                                                                                                                                                                                                         Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1q22, were the marker is linked to a variant form of the SCZ gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arescricascaccarcaresarcriscricerriscerscaaaccrescessaascascrista 104
                                                                                                                                                                                                                                                                                                                                                                                               This sequence was isolated using the method of the invention as the SCZ gene. This sequence has been previously identified as CD84, GenBank Accession No: NM 003874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. The proteins encoded by this sequence may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method comprises determining the presence or absence of an patient. The method comprises determining the presence or absence of an allele of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1422 and is linked to a gene (SCZ) having a variant form associated with a phenotype of schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                  GluValGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly
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GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIle
                                                  GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATC
                                                                                   PheGlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSer
                                                                                                  TTCCAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGGCCCAGAACCCTGTCAGC
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                   The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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human secreted proteins, and encode the proteins given in AAY12521 to human secreted proteins, and encode the proteins given in AAY12521 to AAY12668, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid and sequences can be used for producins secreted human gane products. They can also be used to develop products for diagnosis and therapy. The proliferation/differentiation activity, tell productive hormone crivity, tissue growth regulating activity, themetopolesis regulating activity, chemotactic/ chemokinetic activity, hoemotactic/ chemokinetic activity, themour inhibition activity or other activity, antiinflammatory call activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping promoter. The sequences can also be used for obtaining corresponding promoter.
                                                                                                                                                                                                         MetGluAspAlaGlyAspTyriysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
Human, secreted protein, EST, expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; oytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; antiinflammatory; tumour inhibition; antitumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from umbilical cord, lymph ganglia, lymphocytes and placental tissue.
                                                       AlaTyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                                                                TyrryrgluargileHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 748 BP; 246 A; 164 C; 164 G; 171 T; 0 U; 3 Other;
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2000US-0189167P.
2000US-0192099P.
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09-JUN-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0220534P.
                                                                                                                              AAL24045 standard; cDNA; 748
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24-MAR-2000; 2
29-MAR-2000; 2
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Lillie J,

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41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal

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Query Match:

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sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
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SO	SQ Sequence 296 BP; 88 A; 74 C; 64 G; 70 T; 0 U; 0 Other;	296	BP;	88	Ä,	74	່ວ	64	. <u>.</u>	70 T;	0	u;	0	Other;	
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ò	41	41 ValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal 60
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ò	61	61 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHis 78
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TITLE OP INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PC002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER PILING DATE: 1998-03-07
EARLIER FILING DATE: 1998-03-07
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EARLIER PILING DATE: 1997-05-23
US-08-348-792-1

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US-09-435-956A-2

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US-09-435-948-319

US-09-125-4313
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Patent No. 6420526
GENERAL INFORMATION:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 1036, Ap
Sequence 7, Appli
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Sequence 1456, Ap
Sequence 557, App
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13198, A
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    /cgn2_6/ptodatca/l/ina/SB_COMB.seq:*
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6: /cgn2_6/ptodatca/l/ina/PcTUS_COMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-249-016-13198
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RELING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,878
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R FILING DATE: 1997-05-23

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R PILING DATE: 1997-05-23

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R APPLICATION NUMBER: 60/047,614

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RESULT 2
US-09-949-016-1456

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Sequence 1456, Application US/09949016

Sequence 1456, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOU307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/211,755

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

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SPROT PLING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE FOR WINDOWS VERSION 4.0

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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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  NOS: 207012
2 for Windows Version
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100.00%
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                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
; NUMBER OF SEQ ID NOS
; SOFWARE: FastSEQ fo
; SEQ ID NO 557
; LENGTH: 3299
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-557
                                                                                        Alignment Scores:
Pred. No.:
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Batent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-00
PRIOR FILING DATE: 2000-10-00
PRIOR FILING DATE: 2000-10-00
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                                          TyrTyrGluhrgileHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArg
                                                                                      MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr
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           GCTTATGTAACACCAGGAGACTCAGAAACAGCACCGGTAGTTACTGTGACCCACAGAAAT
                                                                                                                                  ThrLygArgTyrAsnLeuGln1leTyrArgArgLeuGlyLysProLys1leThrGlnSer
                                                                                                                                                                              LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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                                                                                                    ACCAAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGT
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US-09-949-016-557
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RESULT 5
US-09-949-016-13198
; Sequence 13198, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLOOU.307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: PSECSE FOR WINDOWS VERSION 4.0
; SEQ ID NO 13198
; LENGTH: 37492
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15683 GTGAAAAAGCTGCAACAGTCAGATGGCTACAGTTTTCTTTTTATGTTCTAGGGCCGGAA 15742
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15983 CTGAGGATGGAAGACGCAGAGACTACAAAGCAGACATAAATACACAGGTGATCCCTAC
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                                                                                    119 ThrThrThrLysArgTyrAsnLeuGlnIleTyrArgArg 131
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Indels:
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Sequence 12299, Application US/09949016

Patent No. 6812339

TERENT NO. 6812339

TITLE OF INVENTION:

TITLE OF INVENTION:

PILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR PLICATION NUMBER: 06/241,755

PRIOR PLICATION NUMBER: 60/241,755

PRIOR PLICATION NUMBER: 60/237,768

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

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PRIOR PLING DATE: 2000-10-03

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                                                  PheProValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThr
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Conservative:
Mismatches:
Indels:
Gaps:
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Best Local Similarity:
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US-09-949-016-12299
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LENGTH: 37475
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TITLE OF INVENTION:

TITLE REPERENCE: P2010P1

CURRENT APPLICANTY 108:123 Human Secreted Proteins

CURRENT APPLICANTY 108:123 Human Secreted Proteins

CURRENT PLING DATE: 1999-01-09

BARLIER PLING DATE: 1999-01-09

BARLIER PLING DATE: 1999-01-09

BARLIER PLING DATE: 1999-01-09

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BARLIER PLING DATE: 1997-07-09

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FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,984
FILING DATE: 1997-08-18
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FILING DATE: 1997-08-18
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FILING DATE: 1997-09-12
APPLICATION NUMBER: 60/058,664
FILING DATE: 1997-09-12
Sequence 53, Application US/09227357
Patent No. 6342581
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Conservative:
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EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER PELICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PALENTIN Ver. 2.0
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Best Local Similarity:
Query Match:
DB:
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JAPELICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOTHARE: FESTSEQ for Windows Version 4.0

LENGTH: 2440
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                                                                              LysGluGluLysAsnValThrTyrAsnTrp-----SerProLeuGlyGluGlu 174
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702 GGGAACCTCACCTACCTACCTG-------GACGAGGAGGTTGACATTAATGGCACT
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807 ACTCAGGACTGTCAGAATGCCCATCAGGAATTCAGA----
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Matches:
Conservative:
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRAESEO FOR Windows Version 4.0

SEQ ID NO 1036
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                                      helysargargalnaspalaalaserlyslysThrIleTyrThrTyrIleMetAlaSerA 269
                                                                                 ------ProArgGlnValLysIleIleAlaTrp------ThrSerLysThr 58
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Matches:
Conservative:
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                                                                                                                                                        269 rgAsnThrGlnProAlaGluSer 276
                                                                                                                                                                                                                                                                                                                     Sequence 1036, Application US/09949016 Patent No. 6812339
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QQ		; Sequence 7, Applicat ; Patent No. 5576423
ò	LeuGlyGluSerValThrPh	; GENERAL INFORMA; ; APPLICANT: A
DP DP	264 GTGGTTAGCATCTCGGGAGTGCCTCTTCAGTTACAACCA 302	, APPLICANT: Chance ; APPLICANT: Cocke
δ	46ThreatgglnValLysllelleAlaTrpThrSerLysThr 58	; APPLICANT: de ; TITLE OF INVER
Dp	303 AACAGCATACAGACGAAGGTTGACAGCATTGCATGGAAGAAGTTGCTGCCCTCACAAAAT 362	; TITLE OF INVENTION ; NUMBER OF SEQUENCE.
ò	59 SerValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHis 78	; CORRESPONDENCY; ADDRESSEE:
QQ	363 GGATTICALCACATATIGAAGIGGGAGAAIGGCTCTTIGCCTTCCAAIACTICCAAI 419	; CITY: Palo Alt
à i	ArgAsnTyrTy	; SIATE: CALLIC ; COUNTRY: USA ; ZIP: 94304-1]
සු (420GATAGATTCAGTTTTATAGTCAAGAACTTGAGTCTTCTCATCAAGGCA 467	COMPUTER READABLE MEDIUM TYPE: F
රු සි	99 LeuArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyr 118 	; COMPUTER: IBM ; OPERATING SYSTE
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දු සු	119 INTINTINTLYBARGYYYASHLEUGINIJETYYANGARGLEUGLYLYBSPOLYSIJETHY 138 525 GITCAGCACGTTCCAGGTTTTTTTTTTTTTTTTTTTTTABAGTTTTABAGTTTTTTTT	; APPLICATION NUM ; FILING DATE: 0
ò	GlnSerLeuMetAlaSerValAsnSerThrCvsAsnValThrT.cnghrCvsGorValGln	ATTORNEY/AGENT IN
qa	GGGCAGGGAAGATCCTGGACAGAGGAAGATGCCAAGTGGCTCTGTCTTGCTTG	REGISTRATION NO REFERENCE/DOCKE
ζ	GluGluLysAsnVe	; TELECOMMUNICATION ; TELEPHONE: 415
qq	::: ::: :: 645 AGGCATGGCAATGTGTTTGGTACAGAGGAGCAAGCTGATCCAGACAGCA 701	; TELEPAX: 415-4 ; INFORMATION FOR SEC
ζ	LeuGlnIlePheGlnThrProGluAspGlnGlu	ĦΞ
Dp	702 GGGAACCTCACCTACCTGGACGAGGTTGACATTAATGGCACT 746	SE
ò	190ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnAsnSerAspSerIleSerAla 208	, TOPOLOGY: line ; MOLECULE TYPE: c
qq	747 CACACATATACCTGCAATGTCAGCAATCCTGTTAGCTGGGAAAGCCACACCCTGAATCTC 806	; FEATURE: ; NAME/KEY: CDS
δ	209 ArgGlnLeuCysAlaAspIleAlaMetGlyPheArgThrHisHisThrGlyLeuLeuSer 228	; LOCATION: 1 US-08-348-792-7
DP PP	807 ACTCAGGACTGTCAGAATGCCCATCAGGAATTCAGA	Alignment Scores:
à	229 ValLeuAlaWetPhePheLeuLeuValLeuIleLeuSerSerValPheLeuPheArgLeu 248	Score:
Op Op	843TITIGGCCGTTTTTGGTGATCATCGTGATTCTAAGCGCACTGTTCCTTGGCACCCTT 899	
λō	249 Phe	Query Match: DB:
Db	900 GCCTGCTTCTGTGTGTGGAGAAAGAGAAGAAGAGAAGCAGTCAGAGACCAGTCCCAAG 959	US-09-882-171-483 (1
ολ	260ThrlleTyrThrTyrlleMetAlaSerArgAsnThrGlnProAla 274	Qy 12 CysLeuGl
DP	960 GAATITITGACAATITJACGAAGATGTCAAGGATCTGAAAACCAAGAGAAATCACGAGCAG 1019	Db 129 TGCCTGTG
λ̈́o	275 GluyerArglleTyrAspGluIleLeuGlnSerLysVal 287	Qy 32 IleLeuGl
og Q	1020 GAGCAGACTITICCIGGAGGGGGGAGCACCAICÍACICIAIGAÍCCAGICCCAGICTICI 1079	Db 180 CAGTTGG
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                     171
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                                                                                                                                                                                                                                                                                                                                                                                  -----GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SerSerValPheLeuPheArgLeuPheLysArgArg-------GlnAsp 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 AlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg------ 269
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                                                                                                                                                                                        120 ThrThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIle 137
                          310 ATAGTGTCTCTTGATCCATCCGAAGCAGGCCCTCCACGTTATCTAGGAGATCGCTACAAG 359
                                                                                            360 TTTTATCTGGAG------AATCTCACCCTGGGGATACGGAAAGC 398
                                                                                                                         ArgMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThr 119
                                                                                                                                                                                                                                                       ThrGlnSerLeuMetAlaSerValAgnSerThrCygAsnValThrLeuThrCygSerVal 157
                                                                                                                                                                                                                                                                                                                                                                                                      ValalaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg
                                                            80 AsnTyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeu
                                                                                                                                                                                                                                                                         507 AAAGTITIAAACAAGACCCAGGGAAGAAGGGACCTGCACCTTGATACTGGGCTGCACAGTG
                                                                                                                                                                                                                                                                                                                     GluLysGluGluLysAsnValThrTyrAsnTrpSer--------ProLeu
                                                                                                                                                                                                                                                                                                                                       -----HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu
                                                                                                                                                          399 AGGAAGGAGGATGGGATGGTACCTTATGACCCTG------GAGAAAATGTT
                                                                                                                                                                                                                       447 TCAGTTCAGCGCTTTTGCCTGCAGTTGAGGCTTTATGAGCAGGTCTCCACTCCAGAAATT
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis-------
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Patent No. 5977303
GENERAL INFORMATION:
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399 AGGAAGGAGGATGAGGATGGTACCTTATGACCCTG------GAGAAAATGTT 446
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CURRENT APPLICATION DATA:
FLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
                                                                                         ZIP: 94304-1104
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
901 California Avenue
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3.02e-14
195.50
39.88%
23.46%
11.53%
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-09-199-955-7
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                                                                                                             -----GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu 189
                                                                                                                                                                                                               190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArg 209
                                                                                                                                                                                                                                                                                                         744 CCCGGAİĞC-------AĞĞAĞAĞACCCCTCAGAACAAACCATGG 782
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                                                      ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal
                                                                                             -----ProLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09199955

Patent No. 6372899

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de vites, Jan E.
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
INVERS OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                          GluLysGluGluLysAsnValThrTyrAsnTrpSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1056 GTG 1058
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129 TCCCTGTGTGAGTGG------GGTGGGCGTGATGAAGACTGCCCAAAGATTCTCCGG 179
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-952-9196
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1079
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Mismatches:
Indels:
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                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                          3.02e-14
195.50
39.88%
23.46%
                                   LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 415-496-1200
                                                                                                                                                 153..1073
                                                                                                MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-880-875-7
                                                                                                                                                                                                Alignment Scores:
 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                            284 GlnSerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGlu 301
                                                                                                                                                                                                                                          843 CAG------TTGAGAAGAAGAAGAAGAAGAAGAACGAACCATTACCAGACA 881
624 AACCCAGCCAACAGCTCCCACCTCCTGTCCCTCGGCCCCCCAGCATGCTGACAAT 683
                               190 ThrTyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArg 209
                                                -------AĠĠĀĊĀĠĀCCCCTCAGAAACCATGG
                                                                                                                                                                   241 SerSerValPheLeuPheArgLeuPheLysArgArg-------GlnAsp
                                                                                                                                                                                                                                                                                         942 AAGAAACTIGACTCCCTGCGCCTGCGACCCTTGCACCACCATGTATAT-----GTIGCT
                                                                                                                                                                                                                                                                       255 AlaAlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg-------
                                                                                       210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis------
                                                                                                                                                    -----HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeu ::: ||||:::||||:::||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Janis G.
APPLICANT: Geron J.
APPLICANT: An E.
TITLE OF INVENTION: FURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
PILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436K
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/0880875
Patent No. 6199065
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                         CCCGGATGC
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                                                                                                                                                       223
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744 CCCGGATGC-----AGGACAGACCCCTCAGAAAAAAAAGAACATGG 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GlyGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeu 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 TTTTATCTGGAG------AATCTCACCCTGGGGATACGGGAAGC 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrGlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal 157
                                                       129 recerenceagres-----egrescecarsarcaececaaagarreteces 179
                                                                                                                                                                                                                                                                       300 ATAGTGTCTTTGATCCATCCGAAGCAGGCCCTCCACGTTATCTAGGAGATCGCTACAAG 359
                                                                                                                                                                                                                                                                                                                                             60 ValAlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AsnīyrīyrGluArgIleHisAlaLeuGlyProAsnīyrAsnLeuValIleSerAspLeu 99
                                                                                                                     --- ValAsnIleGlnGluPro 46
CysLeuGlnThrTrpProGluAlaAlaGlyLysAspSerGluIlePheThrValAsnGly 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    624 AACCCAGCCAACAGCTCCCACCTCCTCACCCTCGGCCCCCAGCATGCTGACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GlnLeuCysAlaAspIleAlaMetGlyPheArgThrHis-------
                                                                                                                                                                            47 ArgGlnValLysileIleAlaTrpThrSerLysThr-------
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285 SerLysValLeuProSerLysGluGluProValAsn-----ThrValTyrSerGluVal 302
                                                                                                                                                                                                                                                           242 SerValPheLeuPheArgLeuPheLysArgArg--------GlnAspAla 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||||::::::
877 GTGGAAAAAAAAAGCCTTACGATCTATGCCCAAGTCCAGAAACCAGGTCCTCTTCAGAAG 936
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                                                                            121 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 138
                                                                                                                                                                                                                                     LysGluGluLysAsnValThrTyrAsnTrpSer--------ProLeu--- 171
                                                                                                                                                                                                                                                                                                                 172 ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 190
                                                                                                                                                                                                                                                                                                                                          619 CCAGCCAACAGCTCCCACCTCTGACCTCGGCCCCCAGCATGCTGACAATATC 678
                                                                                                                                                                                                                                                                                                                                                                                                                        739 GGATGC-------AGGACAGACCCCTCAGAAACAAAACCATGGGCA 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------TTGAGAAGAGGCTAAAACGAACCATTACCAGACAACA 876
                                                                                                     139 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 158
                                                                                                                                                                               TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGln 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 ---HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeuSer 241
  101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
                                       ---GAGAAAATGTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 LeuCygAlaAspIleAlaMetGlyPheArgThrHis-------
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Patent No. 6372899

GENERAL INFORMATION:

APPLICANT: Aversa, Gregorio

APPLICANT: Cocke, Benjamin G.

APPLICANT: Cocke, Benjamin G.

APPLICANT: Gel Vries, Jan E.

TITLE OF INVENTION: FURIFIED GENES ENCODING MAMMALIAN CELL

TITLE OF INVENTION: SURFACE ANTIGENS: PROTFINS AND ANTIBODIES

NUMBER OF SEQUENCES: 12

CORRESPONDENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AlaSerLysLysThrIleTyrThrTyrIleMetAlaSerArg----
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ZIP: 94304-1104

MODIVER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                       394 AAGGAGGATGAGGATGGTACCTTATGACCCTG-
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901 California Avenue
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STREET: 901 Califor
CITY: Palo Alto
STATE: California
COUNTRY: USA
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APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan B.
TILLE OF INVENTION: FURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Resorters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnValLysilelleAlaTrpThrSerLysThr------
                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.25
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-882-171-483 (1-329) x US-08-462-738-1 (1-1716)
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Matches:
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                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-UN-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
RECISTRATION NUMBER: 34,090
RECISTRATION NUMBER: 34,090
RECISTRATION NUMBER: 34,090
RECISTRATION NUMBER: 34,090
TELECOMMUNICATION INFORMATION:
TELEPOMER: 415-496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 base pairs
                                                                                                                                                                                                      3: DNAX Research Institute
901 California Avenue
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40.62%
23.75%
11.44%
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CITY: Palo Alto
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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STRANDEDNESS: single
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Best Local Similarity:
Query Match:
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Pred. No.:
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, LOCATION:
US-08-462-738-1
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101 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 CCAGCCAACAGCTCCCACTCTCCTCACCCTCGGCCCCCAGCATGCTGACAATATC 678
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76
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112
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 02-DEC-1994
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTATION NUMBER: DX0436GC
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER: US/09/199,955
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194.00
40.62%
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; LOCATION: 61..1065
US-09-199-955-1
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MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
Query Match:
DB:
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191 TyrThrCygThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSerAlaArgGln 210 	lis	AGGACAGACCCTCAGAAACAAAACATGGGCA	HisThrGlyLeuLeuSerValLeuAlaMetPhePheLeuLeuValLeuIleLeuSer	778 GTGTATGCTGGGCTGTTAGGGGGGTGTCATCATCATCATGGTGGTAATACTACAG		TTGAGAAGAAGGTAAAACGAACCATTACCAGACAACA	256 AlaSerLysLysThrlleTyrThrTyrlleMetAlaSerArg		SerArgileTyrAspGluIleLeuGln	937 AAACTIGACTCCCTCCCAGGACCCTIGCACCACATATATGTIGCTGCC	SerLysValLeuProSerLysGluGluProValAsnThryalTyrSerGluVal	
oValSerAsnA ::: TATCAGCAACA	LeuCysAlaAspIleAlaMetGlyPheArgThrHis-	AGGACAG	lLeuAlaMetP	TGTCATCATGA	242 SerValPheLeuPheArgLeuPheLysArgArg-	GAGAAGAAGAG	rTyrileMetA	CTATGCCCAAG	!	: GGACCCTTGCA	uGluProValA	ccaggaaacaa
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Search completed: February 5, 2005, 11:31:47 Job time : 239.449 secs

Sequence 1885, Ap Sequence 174, App Seguence 174, Sequence 174,

Description Sequence Sequence Sequence Sequence 1

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ALIGNMENTS

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Sequence 29, Application US/10436523
; Sequence 29, Application US/10436523
; Publication No. US20030180888A1
; GENERAL INFORMATION:
    APPLICANT: Fraser, Christopher C.
    TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
    TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
    CURRENT APPLICATION NUMBER: US/10/436,523
    CURRENT FILING DATE: 2003-05-12
    PRIOR FILING DATE: 2001-11-20
    PRIOR FILING DATE: 2000-11-03
    NUMBER OF SEQ ID NOS: 100
    SOPTMARE: PatentIn version 3.1
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX.1.00
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/2/pubpna/USO7 PUBCOMB.seq:*
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     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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TYPE: DNA ORGANISM: Homo sapiens SEQ ID NO 29 LENGTH: 1040

SUMMARIES

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RESULT 2
US-10-723-860-1885

i Sequence 1885, Application US/10723860

j Publication No. US20040253606A1

j Publication No. US20040253606A1

j CENREAL INFORMATION:

APPLICANT: Aziz, Natasha

j APPLICANT: Glinblurg, Wendy M.

APPLICANT: Glinblurg, Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for Screening for
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Mismatches:
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Gaps:
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US-10-723-860-1885
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Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
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Matches:
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                    GlyLybaBapSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPhePro
                                                                AlaTyrValThrProGlyAspSerGluThrAlaProValValThrHisArgAsn
                                                                                                                         TyrTyrGluargIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg
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Publication No. US20030049618A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT APPLICATION NUMBER: 2001-03-16
Prior application data removed - consult PALM or fill NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 174
IMMORTHY 3173
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Best Local Similarity:
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US-09-809-391-174
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                   GlulleLeuGlnSerLysValLeuProSerLysGluGluProValAsnThrValTyrSer
                                                                                                                                                                                       Sequence 174, Application US/09882171
Publication No. US20030175858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
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PILE REFERENCE: PZ0022PZ
CURRENT PARICATION WORRER: US/09/882,171
CURRENT PARICATION WORRER: US/09/03/31
PRICE PARICATION WORRER: US/09/149/149
PRICE PARICATION MUMBER: US/09/149/149
PRICE PARICATION MUMBER: US/09/149/149
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PRIOR APPLICATION NUMBER: 60/043,519
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR PLING DATE: 1997-04-11
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Sublication No. US20030225248A1

GENERAL INFORMATION:

APPLICANT: ROSen et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/10/164,861

CURRENT APPLICATION NUMBER: US/09/149,476

PRIOR APPLICATION NUMBER: PCT/US98/04493

PRIOR FILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-03-06

NUMBER OF SEQ ID NOS: 757

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 174

LENGTH: 3173
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       PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,585
PRIOR FILING DATE: 1997-05-23
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PRIOR APPLICATION NUMBER: 60/056, 805
PRIOR PLILING DATE: 1997-08-22
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## Sequence 6219, Application US/10723860
## Sequence 6219, Application US/10723860
## GENERAL INFORMATION:
## APPLICANT: Albert
## APPLICANT: Globurg, Wendy M.
## APPLICANT: Globurg, Wendy M.
## APPLICANT: Globurg, Wendy M.
## APPLICANT: Globurg, Wendy M.
## APPLICANT: Globurg, Wendy M.
## APPLICANT: Globurg, Wendy M.
## APPLICANT: Globurg, Wendy M.
## APPLICANT: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
## TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
## TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
## TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
## FILE REFERENCE: 0082-11-26
## PRIOR RPLIANG DATE: 2003-11-26
## NUMBER OF SEQ ID NOS: 8393
## SOFT NOS: 8393
## SOFT NOS: 6219
## IENGTH: 3326
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TYPE: DNA
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NAME/KEY: SITE
LOCATION: (3119)
OTHER INFORMATION: n equ
FEATURE:
NAME/KEY: SITE
LOCATION: (3121)
OTHER INFORMATION: n equ
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Best Local Similarity:
Query Match:
DB:
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; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3669, 3670, 3671, 3672,
; LOCATION: 3678, 3679, 3680, 3681, 3682,
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13255
                                                         Percent Similarity:
Best Local Similarity:
                                       Scores:
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US-10-198-846-13255

Sequence 13255, Application US/10198846

PUBLICATION NO. US2003009974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Wangy Youzhen
APPLICANT: Wangy Youzhen
APPLICANT: Wangy Youzhen
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREV
TITLE OF INVENTION: THERAFY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PRILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SEQ ID NO 13255

LENGTH: 3687

TYDD: NANA
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                          MetAlaGinHisHisLeuTrpIleLeuLeuLeuCysLeuGinThrTrpProGluAlaAla
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3673, 3674, 3675,
3683, 3684, 3685,
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                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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1695.00
100.00%
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99.94%
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Sequence 12, Application US/09860836B
; Publication No. US20030054002A1
; General INFORMATION:
    APPLICANT: WANDSTRADT, AMY
; APPLICANT: WANDSTRADT, AMY
; APPLICANT: WANDSTRADT, AMY
; APPLICANT: WANDSTRADT, AMY
; APPLICANT: WANDSTRADT, AMY
; TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK
; TITLE OF INVENTION: IN INWINE TOLERANCE
; TITLE OF INVENTION: IN INWINE TOLERANCE
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/204,963
; PRIOR APPLICATION NUMBER: 60/204,963
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
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GAGAAAAGTGTTCTGTACAGCTGGACCCCAAGGAACCCCATGCTTCTGAGTCCAATGGA 620
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ORGANISM: Homo
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LENGTH: 2286
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                                                                                             GluvalGlnPheAlaAspLysMetGlyLysAlaSerThrGlnAspSerLysProProGly.320
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APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget A.;
APPLICANT: THANGAVELU, Kavitha; WARREN, Bridget M.;
APPLICANT: TANG, Y. Tom; DUGGAN, Brendan M.;
APPLICANT: TRAN, Uyen K.; BAUGHN, Mariah R.;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
APPLICANT: FORSYTHE, Ian J.; YANG, Junming;
APPLICANT: MASON, Patricia M.;
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REPRENCE: PF-0925 SUN;
FILE REPRENCE: PC-0925 SUN;
FRICHENT PILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US 60/275,249
PRIOR APPLICATION NUMBER: US 60/216,810
PRIOR APPLICATION NUMBER: US 60/216,810
PRIOR APPLICATION NUMBER: US 60/316,810
PRIOR APPLICATION NUMBER: US 60/316,810
PRIOR APPLICATION NUMBER: US 60/32,977
PRIOR APPLICATION NUMBER: US 60/348,447
PRIOR APPLICATION NUMBER: US 60/348,447
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 20
LENGTH: 1849
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OTHER INFORMATION: Incyte ID No: 7500099CB1
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Publication No. US20040097711A1
GENERAL INFORMATION:
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 TITLE OF INVENTION: Methods of therapy and diagnosis using targeting TITLE OF INVENTION: that express Ly-9 FILE REFERENCE: HYS-68 CURRENT APPLICATION NUMBER: US/10/310,612 CURRENT FILING DATE: 2002-12-04 SOFTWARE: PACHICIN NOS: 2 SOFTWARE: PatentIn version 3.1
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TTGTTTAACACATCCATCATTAGCAAAGAGAGAAAGAAGCAGCAACGGCAGATCCACTC
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US-10-310-612-1
, Sequence 1, Application US/10310612
, Publication No. US20040109862A1
, GENERAL INFORMATION:
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APPLICANT: Emtage, Peter

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Sequence 75, Application US/10436523

Sequence 75, Application US/10436523

Publication No. US20030180888A1

GENERAL INFORMATION:

APPLICANT: Fraser, Christopher C.

TITLE OF INTENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

FILE REPERBNCE: 7853-244-999

CURRENT FILING DATE: 2003-05-12

PRIOR APPLICATION NUMBER: US/10/007,303

PRIOR PILING DATE: 2001-11-20

PRIOR PILING DATE: 2000-11-03

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin version 3.1
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Publication No. US20040109863A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Wethods of therapy and diagnosis using targeting of cells
TITLE OF INVENTION: that express Ly-9
FILE REFERENCE: HYS-680P
CURRENT APPLICATION NUMBER: US/10/328,538
CURRENT APPLICATION NUMBER: 10/310,612
PRIOR PAPLICATION NUMBER: 10/310,612
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                             PheArg------LeuPheLysArgArgGlnAspAlaAlaSerLysLysThrlleTyr 262
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817 CCAGTCACCCTGCCACTTGCACTCCCAGCCTGCCGGGACACACAGAAGGTTGTCTGGTTG
                                                                               43 ileGlnGluProArgGlnValLysIleIleAlaTrpThrSer---LysThrSerValAla
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; ORGANISM: Homo sapiens
US-10-328-538-1
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140 SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 159
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                                                                                                                                                                                            60 ValalaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArg 79
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205 CCCCTGGAAATACCACCAGATGAAGAGTTGAGAACATCATCTGGTCCTCTCACAAAGT
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                                                                    US-09-882-171-483 (1-329) x US-10-436-523-74 (1-1139
 Mismatches:
Indels:
Gaps:
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GENERAL INFORMATION: APPLICANT: Ward, Neil Raymond APPLICANT: Mundy, Christopher Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 AsnThrGlnProAlaGluSer 276
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TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
THE REPREBENCE: 7853-244-99 (s/10/436,523
CURRENT APPLICATION NUMBER: US/10/007,303
PRIOR APPLICATION NUMBER: US/10/007,303
PRIOR PLILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR FILING DATE: 2000-11-03
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Percent Similarity:
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US-10-436-523-74
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APPLICANT: No. US20030124575Alartis AG
APPLICANT: No. US20030124575Alartis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: No. US20030124575Alartis Erfindungen Verwaltungsgesellschaft m.b.H.
APPLICANT: Plares, William
APPLICANT: Jaritz, Markus
APPLICANT: Lapp, Hilmar
APPLICANT: Lapp, Hilmar
APPLICANT: Ralthoff, Frank Stephan
ITILE OF INVENTION: Organic Compounds
FILE REPREENCE: 4-31347 PCT
CURRENT APPLICATION NUMBER: US 60/192, 934
FRIOR APPLICATION NUMBER: US 60/205, 026 (US 60/279, 243)
FRIOR APPLICATION NUMBER: US 60/205, 026
FRIOR APPLICATION NUMBER: US 60/205, 026
FRIOR APPLICATION NUMBER: US 60/205, 026
FRIOR APPLICATION NUMBER: US 60/205, 020
FRIOR APPLICATION NUMBER: US 60/205, 020
FRIOR PLING DATE: 2000-05-18
FRIOR PLING DATE: 2000-05-18
FRIOR FILING DATE: 2000-05-18
FRIOR PLING DATE: 2000-05-18
FRIOR APPLICATION NUMBER: US 60/205, 767
FRIOR PLING DATE: 2000-05-19
FRIOR PLING DATE: 2000-05-19
FRIOR PLING DATE: 2000-05-19
ThralaGlnAsnProValSerAsn---AsnSerAspSerIleSerAlaArgGlnLeuCys 212
                                                                      AlaAspIleAlaMetGlyPheArgThrHisHisThrGly------LeuLeuSerVal 229
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SOFTWARE: FastSEQ for Windows Version 4.0
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; LOCATION: (1)...(1423)
; OTHER INFORMATION: n = A,T,C
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                                             APPLICANI: RATIONALI BALLLEY, WILLIAM NIGEL
APPLICANT: RAYLOY, Stuart
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Kingsman, Susan Mary
APPLICANT: Kingsman, Susan Mary
APPLICANT: Kingsman, Susan Mary
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFRENCE: 53262000100
FURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SEQ ID NO 132
LENGTHARE: FRALESEQ for Windows Version 4.0
SEQ ID NO 132
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                                     Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
   Robert Alan
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; ORGANISM: Homo Sapiens
US-10-170-385-132
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                                                              40 provalAsnileGlnGluProArgGlnvalLysIleileAlaTrpThrSerLysThrSer 59
20 AlaGlyLysAspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPhe 39
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Mus muscu 603063795 Mus muscu BX388160

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 987)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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VIRTUAL TRANSCRIPT, partial sequence,
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-MODEL=frame+ p2n.model -DEV=x1h
-QDESE_frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_epool/USO9882171/runat_04022005_1144004_26033/app_query.fasta_1.910
-Q=/cgn2_1/USPTO_epool/USO9882171/runat_D402605_114004_26033/app_query.fasta_1.910
-Q=/cgn2_1/USPTO_epool/USO9882171/runat_D402603
-UNITS=bits -TART=1 -END=1 - MATRIX=blosum62 - TRAMS=humand.cdi_-LIST=45
-DOCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -MAXLEN=200000000
-USER=USO9882171_GCGG1 1 4385_GTUNAT_04022005_1144004_2603_3 -NCPU=6 -ICPU=3
-UNO MMAP -LARGEQUERY -NEG_SCORES=0 - WAIT - DSPENCCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Database

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Result

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AL561522

AL561509

Homo sapi BP300475

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AY408982

Pan troglodytes CD84 gene, VIRTUAL TRANSCRIPT, partial sequence, AY408982
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Direct Submission

L Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers

L. 987

I. 987

I. 987

Amol Lype="genomic DNA"

Amol Lype="genomic DNA"

Amol Lype="genomic DNA"
                                                               Pan troglodytes (chimpanzee)
Pan troglodytes
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (Dases 1 to 987)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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                                                                                                                    987
328
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0
                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<li...>987
/gene="CD84"
/locus_tag="HCM3405"
                                                                                                                                                                                                              US-09-882-171-483 (1-329) x AY408981 (1-987)
                                                                                                                  4.06e-190
1695.00
100.00%
100.00%
99.94%
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Best Local Similarity:
Query Match:
DB:
                                                                                                         Alignment Scores:
Pred. No.:
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/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR23 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
                                                                                               Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA
1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA
1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA
1 Jimmy Fund May Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5380
Fax: 617 632 5380
Email: Marc Vidal Géri. harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers
FORWARD: ATGGCTCAGCCACCTA
BACKMARD: ATGGCTCAGCACTCAAGT
INSERT Length: 608 Std Error: 55.00
Plate: 11032 row: 11 column: E
Seg primer: ACTGCCCTCTTTTACAAGCTCGTGAACTGGGAAAAC
High quality sequence start: 91
High quality sequence start: 91
High quality sequence store 607
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Dricct, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
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Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
                                                 80
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                                                                                                   ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSer
                                                                                                                                                                                                                                                                                       GluLysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyGsnValLeuGlnIle
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     GTAAATATCCGAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAAACTCTGTT
                                               AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                      GCTTATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CV023928 608 bp mRNA linear EST 20-AUG 1001 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC020063, mRNA sequence. CV023928 CV023928.1 GI:51481736
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1 (bases 1 to 608)
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582 bp mRNA linear EST 17-SEP-2004 ary, macrophage Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                gMetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrTh 120
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1 (bases 1 to 582)

Suzuki, Y., Yamaabita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Squence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                  50 ATGCTCAGCAGCCACCTATGGATCTTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGC
                                                                                                                                                          170 TGTAAATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGT
                                                         1 MetalaGlnHis-HisLeuTrpIleLeuLeuCysLeuGlnThrTrpProGlualaAl
                                                                                                                                                                                                          OValAsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVa
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Homo sapiens
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B. 1 (Bases 1 to 1074)

B. 1 (Bases 1 to 1074)

B. NIH-MGC http://mgc.nci.nih.gov/.

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis Staudt, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

Plate: LLAM10068 row: b column: 14

High quality sequence stop: 638.
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-langth clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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602291349F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385965 5',
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                                                                                                                                 LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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                                                               Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                   Clark, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G. (Janowski, S., Nielson, R., Iu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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1 (bases 1 to 923)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, F.
Todd, M.A., Tanenbaun, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11eAlaTrpThrSerLysThrSerValAlaTyrValThrProGlyAspSerGluThrAla
        Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..582
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Mus musculus CD84 gene, VIRTUAL, '
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 535)
Dias Neto,E., Garcia (Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.
                                                                                                                                                                                                                                                                             90 GGAAGCGACACAGACATCTTCATAGTGAATGGGATTCTGGGGGAGTCAGCTATTTCCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetGluaspalaglyaspTyrLysalaaspIleasnThrGlnalaaspProTyrThrThr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 220
                                                                                                                                                                                                                                                                                                                                                            MetAlaGlnHisHisLeuTrplleLeuLeuCysLeuGlnThrTrpProGluAlaAla
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S Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTS from pooled-tissue normalized libraries of bovine ESTS from pooled-tissue normalized libraries ochact: Smith TPL USDA, ARS, US Meat Animal Research Center

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                                                                                                                                                                                                                                                                                                   114 AAGAAAACAGTATATGCTGTAGTT-----TCAAGAAATGCTCAACCCACAGAGTCCAGA
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Bos taurus (cow)
Bos taurus
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EST 10-JAN-2001 mRNA sequence.

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                                                                                                                                                                                     Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CT0547-09100-001-a04&t3=2000-00-09&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence start: 7

High quality sequence stop: 533.
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//mol type="mmx" "more."
//mol type="mmx" "mon: 19606"
//dev stage="Adult"
//clone_lib="Crolon; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                   Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Sus scrofa (pig)
Sus scrofa (pig)
Sus scrofa (pig)
Sus scrofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Suina; Suidae; Sus.
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 837)
Sus scrofa
1 (bases 1 to 837)
Sus scrofa; Manasima, N. and Awata, T.
Suchi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Gumitai, N., Hamasima, N. and Awata, T.
Subrace (Prom porcine full-length cDNA libraries
Autocact: Hirohide Uenishi
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Fax: +81-29-638-8627
Fax: +101-29-638-8627
Fax:
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/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
thymus"
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Low quality bases were trimmed based on the quality values.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP159730 Full-length enriched swine cDNA linear EST 30-DEC-2003 BP159730 full-length enriched swine cDNA library, adult thymus Sus scrofa cDNA clone THY010074A04 5', mRNA sequence.
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                                          454
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                                                                                                                                                      395 CACCAAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAG
                                                                                                                rLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGl
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/organism="Sus scrofa"
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BP159730.1 GI:40409203
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                                                                                       294
                                                                                                                                                                        MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAla---AspProTyrThr 119
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                                                           80
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Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical. Science, University of Tokyo
4-6-1, Shirokamedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
                   TTAAGTATCCTCAAATCAGAAGAAGTTAAAAGTATTCCTGGAATTCCAAAACATCTGTC
                                                                        GTCAGCAACAATTTGTGACTCCATCTCTGCCCAGCAGCTCTGTGCAGACATCGCAGTGGGC
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                                                        AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
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                                                                                                                                                                                                                                                                                                      CGGAGTTTAATGACATCTATGAATGGCACCTGTAATGTCACACTGACATGCTCTGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValSerAsnAsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGly
                                                                                                                                                                                       ACCATCACTAAGTGCTTCAACCTTCAAGTCTATCGTCGGCTTGGGAAGCCAAAAATTACT
ValAsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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Homo sapiens (human)
Homo sapiens
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BP303194
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BI151764 1788 bp mRNA linear EST 05-JUL-2001
602915927F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5066478 5',
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                               113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrLysArgTyrAsnLeuGlnlleTyrArgArgLeuGlyLysProLysIleThrGlnSer 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 ACCAAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATT-ACACAGAGG 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 TATTATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uGluLysAsnValThrTyrAsn-TrpSerProLeuGlyGluGlu 174
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3
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Matches:
Conservative:
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Mus musculus
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818.00
94.89%
93.18%
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/done="Invasion: 1900"
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/lab hote="Wixed (pool of 40 RNAs)"
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/clone lib="Wix MGC 126"
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Site 2: Sfil (ggccgctcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidnney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salitary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-ATCTAGAGGCGCAGGGCGCGACTAGGGCGGG-3' and 5'-ATCTAGAGGCGGAGGGCGCGACTAGGTGGCGGGGGGCGCGATAGGGCGGG-3' and 5'-ATCTAGAGGCGGAGGGGCGCAATAGGGCGGG-3' and 5'-ATCTAGAGGCGAGGGGCGCGAATG-4T(30)NN-3'. Pull-length enriched library was constructed using the Clontech creator SNART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH MGC 127 and NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH MGC 127 library."
                                                                                                                                                                                                                                 BUYZ/YY6 466 bp mRNA linear EST 18-OCT-2002
AGENCOURT 10434334 NIH MGC 126 Homo sapiens cDNA clone
IMAGE:6653558 5', mRNA sequence.
                                                      224 rGlyLeuLeuSerValLeuAlaMetPheLeuLeuValLeuIleLeuSerSerValPh 244
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 46)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov m column: 14
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Location/Qualifiers
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Homo sapiens
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/clone="IMAGE:5066478"
/tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin...
/lab host="DH108"
/clone lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Torgan: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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  Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11179 row: e column: 07 High quality sequence stop: 782. Location/Qualifiers
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36
59
6
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
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Query Match:
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Exploration Research Genome Encyclopedia Project of Genome Exploration Research in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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/clone_lib="RIKEN full-length enriched, NOD-derived CD11c
+ve dendritic cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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                                                                                                                                                                               Contact: Yoshihide Hayashizaki
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of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
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/strain="NOD"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musi
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NCI CGAP Subl library is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI CGAP Libraries. NCI CGAP CO4, NCI CGAP Pr28, NCI CGAP CO4, NCI CGAP Pr22, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI CGAP LA12, NCI 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dr track that was present in the
oligonuclectide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINN at:
                                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                                                                                                                                                       MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 120
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                                                                                                                                                                                                                                    TATAAAGGACGAATAGAAATCATAGATCAGAAGTATGACCTGGTCATTAGAGACCTGAGG
                                                                                                                                                                                                                                                                                                                                       ATGGAAGATGCAGGAACTTACAAAGCAGACATCAATGAAGAAATGAGGAA---ACCATC
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                                                                                             AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                                                                 |||:::::: |||||| ::::::
205 GCTTTTATAAAACCAGGAGTCAATAAAGCTGAA----GTTACCATAACCAGGGCACT
                                                                                                                                                                                           TyrTyrGluArgileHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArg
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Homo sapiens
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AUTHORS
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                                                                                                                                                                                                                                                         Homo sapiens (human)

Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.

I (bases 1 to 389)

SINI-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov/

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

CONA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M. A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: MIJ Forward.

Location/Qualifiere

1. 1899
                        389 bp mRNA linear EST 16-FEB-2000 UI-HF-BMO-adu-d-01-0-UI.rl NIH_MGC_38 Homo sapiens CDNA clone AW408076
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VERSION
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nrustal/ 967 bp mRNA linear PRI 01-JAN-2000
Homo sapiens leukocyte differentiation antigen CD84 isoform CD84d
(CD84) mRNA, complete cds.
                                                                       BD191209 186 human
AX224719 Sequence
BC020063 Homo sapi
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AX474326 Sequence
AX474314 Sequence
AX474332 Sequence
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BC074754 Homo sapi
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 967).
Palou, E., Sole, 7, Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapi
Homo sapi
Sequence
                   Y12632 H.sapiens m
AF054816 Homo sapi
                                                        U96627 Homo sapien
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AX474313 Sequence
AF275725 Homo sapi
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AX474331 S
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AX474323 S
AX474326 S
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AC012471
AC027082
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AC3314
CQ718717
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AC144333
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AF054817
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-MODBL=frame+ p2n.model -DEV=xlh
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CR541847 Homo sapi
AX474268 Sequence
U82988 Human leuko
                                                                                                                                             Pebruary 5, 2005, 03:24:06 ; Search time 3491.17 Seconds
   (without alignments)
   2761.994 Million cell updates/sec
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Compugen Ltd.
                                                                                                        nucleic search, using frame_plus_p2n model
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                       GenCore version
Copyright (c) 1993 - 2005
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Listing first 45 summaries
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Xgapop 10.0, Ygapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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www.rzpd.de/cgi-bin/products/showlib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD,
Contact RZPD (customer.service@rzbd.de) for further information.
This cDS clone is part of a collection of human full ORP clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GGC TCC ACC (ARG).
The last codon is followed by the 3' att site: GACCCAGCTTTCT. att
The clone is validated by full sequence check.
Compared to the reference sequence NM 003874 (GI:4502686) we found
AAA exchange(s) at position (first base of changed triplet):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /processin_id="CAG46645.1"

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www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDO834H0132D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                           Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J. Cloning of human full open reading frames in Gateway (TM) system
                                                                                                                                                                                                                                                   Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
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Clone distribution: http://www.rzpd.de/products/orfclones/
Location/Qualifiers
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Mismatches:
Indels:
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Matches:
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/db xref="taxon:9606"
/clone="RZPDO834H0132D"
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                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-JUN-2004) RZPD
                                                                                                                                                        entry vector (pDONk201)
Unpublished
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Direct Submission
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BAGDYKADINTQADPYTTTRXTNLQTYRRLGGREVTTOGLMESVNSTCRVTTCCSVEKE
EKNVTYNWSPLGEBEGNLQIFGTPEDQELTYTCTAQNPOSNNSDSISARQLGADIAMG
PRTHHTGLLSVLAMFFLLVLILSSVFLFRRRRQGASLQGRASEHSLFRSAVC"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 TATGTAACACCAGGAGACTCAGAAAACAGCACCCGTAGTTACTGTGGACCCACAGAAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 AATAICCAAGAACCACGGCAAGTTAAAAICATTGCTTGGACTTCTAAAACAICTGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 TATGAAGGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGGGATCTGAGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 GAAGACGCAGGAGACTACAAAGCAGACATAAAATACACAGGCTGATCCCTACACACCACCACC
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CR541847.1 GI:49456648
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Homo sapiens (human)
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( Dases 1 to 1040)

de la Fuente, M.A., Pizcueta, P., Nadal, M., Bosch, J. and Engel, P. CD84 leukocyte antigen is a new member of the Ig superfamily Blood 90 (6), 2398-2405 (1997)
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2 (bases 1 to 1040)
de la Fuente,M.A., Pizcueta,P. and Engel,P.
Direct Submission
Submitted (21-DEC-1996) Hepatology, Fundacio Clinic, Villarroel
170, Barcelona 08036, Spain
Location/Qualifiers
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                                                                                                                             61 TyrGluhrgileHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArgMet
                       LyshapSerGluIlePheThrValhanGlyIleLeuGlyGluSerValThrPheProVal
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CD84 mRNA, complete cds.
US-09-882-171-483_COPY_22_220 (1-199) x AX474268 (1-1040)
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/cell_line="Raji; B cell line"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="1"
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Human leukocyte antigen
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       21 AsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                           1 LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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Cd2000 and cd2001 molecules and uses thereof
Cd2000 and cd2001 molecules and uses thereof
Patent: BP 1223218-A 29 17-JUL-2002;
Millennium Pharmaccuticals, Inc. (US)
Location/Qualifiers
1. .1040
/ organism="Homo sapiens"
/ mol type="unassigned DNA"
/db xref="taxon:9606"
    US-09-882-171-483_COPY_22_220 (1-199) x CR541847 (1-984)
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Gaps:
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CD84c"
                          Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1067)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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Gaps:
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RIYDEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIVI"
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Homo sapiens (human)
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                                                                  81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
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                                                                                                                                                                                                                                                                                          GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servel d'Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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CD84a"
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1118 bp mRNA linear PRI 01-JAN-200
Homo sapiens leukocyte differentiation antigen CD84 isoform CD84a
(CD84) mRNA, complete cds.
AF054816
 80
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                     313 TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG
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TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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L. Unpublished
L. Unpublished
CE 2 (bases 1 to 1100)
JRS Gaya, A.
B Direct Submission
S. Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Villarroel 170, Barcelona 08036, SPAIN
Location/Qualifiers
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133. .1086
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H.sapiens mRNA for leukocyte differentiation antigen CD84.
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leukocyte differentiation antigen.
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Ruben, S.M., Rosen, C.A., Fischer, C.L., Soppet, D.R., Carter, K.C., Bednarik, D.P., Endress, G.A., Yu, G.L., N, J., Feng, P., Young, P.E., Grene, J.M., Ferrie, A.M., Duan, R., Hu, J.S., Florence, K.A., Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y.,
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BD191209.1 GI:33000948
JP 2002510192-A/173. unidentified unidentified
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1299)
Palou,E., Freed,J.H., Sole,J., Pi,A., Vilella,A., Vives,J. and
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Submitted (07-APR-1997) Servei Immunologia, Hospital Clinic,
Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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                                                                              GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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         LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
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Matches:
Conservative:
Mismatches:
Indels:
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C12N1S/12,C12NS/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/68,
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Matches:
Conservative:
Mismatches:
Indels:
Lafleur, D.W., Li, Y., Zeng, Z. and Kyaw, H. 186 human secreted proteins Parent: JP 2002510192-A 173 02-APR-2002, HUMAN GENOME SCIENCES INC
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                 TITLE
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Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 26 Row: o Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447
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Conteact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Submitted (19-DEC-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                          474 ATGGCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAGAAGAA
                                                                                                               141 LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu
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Catarrhini; Hominidae; Homo.
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LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
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Submitted (05-FEB-1998) Krause S.W., Hematology, University of
Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042,
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cell surface antigen; glycoprotein; MAX.3 antigen.
Homo sapiens (human)
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Homo sapiens mRNA for MAX.3 cell surface antigen.
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/product="MAX.3 cell surface antigen"
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                   LysAsnvalThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                             508 AAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATCTTC
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Matches:
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Indels:
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PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               Sequence 4648 from Patent W002068579.
CQ718714

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AF043445 1132 bp mRNA linear ROD 16-MAR-1999
Mus musculus CD84 leukocyte antigen (CD84) mRNA, complete cds.
AF043445
AF043445.1 GI:4105142
                                                                 /protein_id="AAP21724.1"
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PSLLVSLRDHSEELGGLAVGHIL"
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CD84s"
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AF054818 GI:6650111
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1 (bases 1 to 858)
Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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                                                                                                                   1 LysaspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                 21 AsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerValAla
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Matches:
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                  5.51e-104
1039.00
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Homo sapiens
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                                           Percent Similarity:
            Alignment Scores:
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de la Fuence, M.A., Tovar, V., Pizcueta, P., Nadal, M., Bosch, J. and Engel, P.
Molecular cloning, characterization, and chromosomal localization of the mouse homologue of CD84, a member of the CD2 family of cell surface molecules
Immunogenetics 49 (4), 249-255 (1999)
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           Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                           Gases 1 to 1132)

de la Fuente, M.A., Tovar, V., Pizcueta, P. and Engel, P.

Direct Submission
Submitted (17-JAN-1998) Immunology Unit, Department of Cellular
Biology, Medical School, University of Barcelona, Casanova 143,
Barcelona 08036, Spain
Location/Qualifiers
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Matches:
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Mismatches:
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musculus (house mouse)
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Search completed: February 5, 2005, 09:29:31 Job time : 3495.17 secs

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version 5.1.6 - 2005 Compugen Ltd.

GenCore (c) 1993

Copyright

nucleic search, using frame_plus_p2n model

protein

Run on: ĕ

US-09-882-171-483_COPY_22_220 1039

score:

Title: Perfect

Sequence:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

4390206 segs, 2959870667 residues

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Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

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Acd82804 cDNA sequ
Adi2289 cDNA enco
Adi73891 thuman sec
Adi82906 thuman sec
Adi823942 PRO polyp
Adi72319 thuman RO
Acq23399 thuman sof
Acq23105 Breast ca
Adi57104 thuman NOV
Adk98595 thuman imm
Adi57102 thuman imm
Ads96363 DNA encod
Aas20420 thuman DNA
                                                                                                                                                                                                                             Ado63781 Human Ly-
Ado78173 Human Ly-
Aad43598 Human CD2
Aad63409 Human CD2
Aad43601 Human CD2
Aad43603 Human CD2
Aad43605 Human CD2
Aad43605 Human CD2
Aad63414 Human CD2
Aad43596 Human CD2
Abv77939 Hypoxia-i
Aad19728 Dendritic
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Aad43604 Human CD2
Aad63415 Human CD2
Ab189654 Human pol
Ada40164 Human sec
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Add7686 Human sec
Ada56325 Gene enco
Add45579 Human CD2
Add43584 Human CD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, immunoglobulin; Ig; SLAM associated protein; SAP; CD2000 protein; immune proliferative disorder; immune disorder; rheumatoid arthritis; carcinoma; autoimmune disorder; multiple sclerosis; Grave's disease; hashimoto; disease; aquired immune deficiency syndrome; hepatotropic; osteoarthritis; allergic inflammatory disorder; viral infection; asthma; psoriasis; apoptotic disorder; systemic lupus erythematosus; bronchitis; diabetes mellitus; septic shock; chronic obstructive pulmonary disease; acute myptema; carculatory disorder; hepatitis; circulatory disorder; hepatitis; circulatory disorder; hepatitis; circulatory disorder; immunosuppressive; neuroprotective; antinflammatory; Crohn's disease; osteopethic; antipacterial; immunomodulator; inflammatory; bown's disease; osteopethic; antipacterial; immunomodulator; inflammatory; when a
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Aad43584 Human CD2
Aad63395 Human CD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jaundice; dermatological; ulcerative colitis; AIDS; CD84; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Human CD84 protein"
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ABL89654
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AAD43602,
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AAD43605
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AAD43563
            Ado05707 Human leu
Adg19066 Human sof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aav59674 Human sec
Abs73661 Human cDN
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                                                                                                                                   February 5, 2005, 03:16:45; Search time 423.629 Seconds (without alignments) 2780.804 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                          1 KDSEIFTVNGILGESVTFPV.......NNSDSISARQLCADIAMGFR 199
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SUMMARIES

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Query Match Length DB

Score

Result No.

genesequ2002bs:*
genesequ2002bs:*
genesequ2003bs:*
genesequ2003cs:*
genesequ2003cs:*
genesequ2004as:*

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:

Geneseq_16Dec04:* geneseqn1980s:* geneseqn1990s:*

Database

genesegn2004bs:*

AAD43563 ADO05707 ADQ19066 AAV59674 ABS73661

9 5 5 5 6

1040 1067 1067 3173

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                                                                  LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
                                                                                                                                                       140
                                                                                                                                                                                               Argecarcrigicaacaccaccrigiaargicacacrigacarecrigicaragagaaagaagaa 524
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                                                                                                                                                                                                                                                                                                                           GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                                                                                                                                                                                                                                     644
                                                                                                                                                                                                                                                                                   <u>AAGAATGTGACATACAATTGGAGTCCCCTGGGAGAGAGGGGTAATGTCCTTCAAATCTTC 584</u>
                                                                                                                                                                                                                                                                                                                                                                                                               AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGACGCAGGAGATACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACC
                                                                                                               AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGTTTA
                                                                                                                                                                                                                                                                                                                                                   585 CAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCCAGAACCCTGTCAGCAAC
                                                                                                                                                    MetalaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu
                                                                                                                                                                                                                                           LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to treating a subject having a condition that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T cell; antiallergic; immunosuppressive; virucide; antibacterial; antiparasitic; cytostatic; gene therapy; human; gene; CD83; ds; leukocyte differentiation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte differentiation antigen CD84 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; SEQ ID NO 7; 161pp; English.
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; 2002US-0417243P.
; 2002US-0419575P.
; 2002US-0424777P.
; 2002US-0424881P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO05707 standard; DNA; 1067
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09-OCT-2002;
18-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin [1g] and 1g-like domains and SLMA associated protein (SAP) motifis. CD2000 DNA and protein is useful for treating disorder such as immune proliferative disorders. Immune disorders (e.g. carcinoma), viral infection, autoimmune disorders (e.g., arthritis, multiple solerosis, Grave s disease, and Hashimoto's disease), T cell disorder (e.g. arquired immune deficiency syndrome (AIDS)), inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), inflammatory disorders (e.g. rheumator) asthma and osteoarthritis, allergic inflammatory disorders (e.g. sthma and osteoarthritis), allergic inflammatory disorders (e.g. spetum and osteoarthritis), allergic inflammatory disorders (e.g. spetum and not contain and observation and insembly contained broaders, hepatic circulatory disorders, hepatitis, cirrhosis, cachexia, jaundice, hepatic circulatory disorders, hepatitis, cirrhosis, coute myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 DNA
                                                                                                                                                                                                                                                                                                                                                                       like domains and SLAM associated protein, termed CD2000 or CD2001, useful for treating immune, inflammatory, or hepatic circulatory disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
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like domains and SLAM associated protein, termed CD2000 or CD2001, usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 TATGTAACACCAGGAGACTCAGAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 AATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
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Mismatches:
Indels:
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                                                                                                            02-NOV-2001; 2001EP-00309339
                                                                                                                                                         03-NOV-2000; 2000US-00706167
                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
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Best Local Similarity:
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Human soft tissue sarcoma-upregulated DNA - SEQ ID 1885.

26-AUG-2004 (first entry)

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relative to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1, GPR-32, CD83, CD84, CD89, escotomin R BY55, serotomin R2C, GFR63, histamine R.H4, GFR5, EPO-R, PSG-1, PSG-3, PSG-6, PSG-9, PDB-4d, and PI-1-related kinase to the subject, such that treatment occurs. The methods characterized by a too-vigorous or weak effector T cell or regulatory T cell response to antigens associated with the condition, such as in an allergic response, an autoimmune disorder, a virsal infection, a microbial infection, a parasitic infection or a tumour. The present sequence represents a DNA encoding a human leukocyte differentiation CD84 antigen, preferentially expressed in regulatory T cells.
benefits from modulating the balance of regulatory T cell function
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Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;

Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	t Scores: .: Similarity: al Similarity: tch:	8.02e-106 1039.00 100.00\$ 100.00\$ 12	Length: Matches: Conservative: Mismatches: Indels:	1067 1199 0 0 0
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දුර	133 AAAGACTCA	GAAATCTTCACAGTG	aaagactcagaaatcttcacagtgaatgggattctgggagagtcagtc	AGTCAGTCACTTTCCCTGTA 192
۵,	21 AsnileGlr	GluProArgGlnVal	LysileileAlaTrpT	AsnileGinGluFroArgGinValLysilelleAlaTrpThrSerLysThrSerValAla 40
QQ	193 AATATCCAA	GAACCACGGCAAGTT	raaarcatteetreea	AATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCT 252
ò	41 TyrValThr	ProGlyAspSerGlu	ThrAlaProValValT	rValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
QQ Q	253 TATGTAACE	CCAGGAGACTCAGAA	ACAGCACCCGTAGTTA	TATGTAACACCAGGAGACTCAGAAACAGCACCGTAGTTACTGTGACCCACAGAAATTAT 312
ò	61 TyrGluArgIl	IleHisAlaLeuGly	/ProAsnTyrAsnLeuV	eHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArgMet 80
qa	313 TATGAACG	SATACATGCCTTAGG	rccgaactacaatctg	TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG 372
ò	81 GluAspAla	GlyAspTyrLysAla	AASpIleAsnThrGlnA	GluaspalaGlyaspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100
Dp	373 GAAGACGC	AGGAGACTACAAAGCA	AGACATAAATACACAGG	GAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCCACC
ò	101 LYSArgTy	rAsnLeuGlnIleTy1	rArgArgLeuGlyLysE	LygargTyrasnLeuGlnIleTyrArgargLeuGlyLysProLysIleThrGlnSerLeu 120
qq	433 AAGCGCTAC	CAACCTGCAAATCTAT	rcsrcsscttssaaa	AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGTTTA 492
ò	121 MetAlaSer	CValAsnSerThrCys	MetalaSerValAsnSerThrCysAsnValThrLeuThrCysS	SysserValGluLysGluGlu 140
qq	493 ATGGCATC	rgrgaacagcaccrg	ratgreacactgacar	ATGCCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAGAAGAA 552
č	141 LysAsnVa	ThrTyrAsnTrpSe	LygAsnValThrTyrAsnTrpSerProLeuGlyGluGlyGluGlyAsnValLeuGlnI	31yAsnValLeuGlnIlePhe 160
qq	553 AAGAATGT	SACATACAATTGGAGT	rcccrgggagaagagg	AAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATCTTC 612
ò	161 GlnThrPro	GlnThrProGluAspGlnGluLeuThrTyrThrCy	uThrTyrThrCysThrAl	AlaGlnAsnProValSerAsn 180
Db	613 CAGACTCC	rgaggaccaagagctr	SACTTACACGTGTACAC	CAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGCAAC 672
È	181 AsnSerAs	snSerAspSerIleSerAlaArgGlnLeuCysAl	gGlnLeuCysAlaAspIl	
QQ	673 AATTCTGA	crecarereced	scaecrererecaeaez	ANTICTGACTCCATCTCTGCCCGGCAGCTCTGTGCAGCATCGCAATGGGCTTCCGT 729

372

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AsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerValAla

LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal

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Length:
Matches:
Conservative:
Mismatches:

8.02e-106 1039.00 100.00% 100.00%

Alignment Scores:

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US-09-882-171-483_COPY_22_220 (1-199) x ADQ19066 (1-1067)

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81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr 100

TyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet

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ADQ19066 standard; DNA; 1067 BP.

ADQ19066

ADQ19066 ID ADQ1 XX AC ADQ1 XX

RESULT 3

253 TATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAT 312

TyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr

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soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for detecting soft tissue sarcome which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1067 BP; 315 A; 264 C; 238 G; 250 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                  Zlotnik A;
                                                                                                                                                                                                                                                                                                                                          (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                    26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                            26-NOV-2003; 2003WO-US038193
                                                                                                                                                                                                                                                                                                                                                                                  Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-441208/41
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                                                                                                                                          Homo sapiens.
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      Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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                                                LysargTyrasnLeuGlnIleTyrargargLeuGlyLysBroLysIleThrGlnSerLeu 120
                                                                                                                                                                                                                                    GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                             MetalaservalasnserThrCysAsnvalThrLeuThrCysServalGluLysGluGlu 140
                                                                                                                                                                                                                                                                                                LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein gene 164 clone HSAWF26.
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MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn; nervous system disorder; Alzheimmer's disease; infection; corneal infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
                                                                                                                                                                                                        181 AsnSerAspSerIleSerAlaArgGInLeuCyaAlaAspIleAlaMetGlyPheArg 199
                                                                                                                                                          LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                                       Human cDNA #1 for novel secreted protein gene 164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LyshrgTyrasnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120
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                                                                                                                                               Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAspAlaGlyAspTysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
                                                                                                                                                             Brewer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LyshapSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 AATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrGluArg1leHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
                                                                                                                                                                                                                                                                New isolated human genes and the secreted polypeptide(s) they en useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                         Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Gr
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R,
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-882-171-483_COPY_22_220 (1-199) x AAV59674 (1-3173)
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        97US-0057669P.
97US-0057761P.
97US-0058785P.
97US-0061060P.
                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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P-PSDB; AAW74891.
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                                                            02-OCT-1997;
                            05-SEP-1997;
12-SEP-1997;
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The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA contess also given in the specification, encoded by one of 309 cDNA condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrowascular disorders e.g. cardiac arrest, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders c.g. corneal infection. The polypeptides can also be used to aid wound healther an epithelial cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was constant and processed to the printed specification, but was Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; dednarkb DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM; Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA; Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or seqdata.uspto.gov/sequence.html?DocID=6420526B1 Example 1; SEQ ID NO 174; 129pp; English. WPI; 2002-634796/68. P-PSDB; ABG95343. preservative.

BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other; Sequence 3173 Alignment Scores:

3173 1199 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 3.5e-105 1039.00 100.00% 100.00% Best Local Similarity: Query Match: Percent Similarity:

US-09-882-171-483_COPY_22_220 (1-199) x ABS73661 (1-3173)

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120	101 LyskrgTyrasnLeuGln1leTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu 120	101
413	354 GAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCACC 413	354
100	GludspalaGlyAspTyrLysalaAspIleAsnThrGlnAlaAspProTyrThrThr	81
353	4 TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG	294
80	61 TyrGluargileHisAlaLeuGlyProAsnTyrAsnLeuVallleSerAspLeuArgMet 80	61
293	TATGTAACACCAGGAGACTCAGAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAT	234
09	1 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr	41
233	174 AATATCCAAGAACCACGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTTTGCT	174
40	AsnileGinGluProArgGinValLysileIleAlaTrpThrSerLysThrSerValAla	21
173		114
20	1 LysAspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 1	1

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                                     23-MAY-1997
  Whuman, secreted protein; hyperproliferative disorder; leukaemia;

Wheast cancer; wound; reproductive disorder; blood-related disorder;

Wheemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;

Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

Wiskott-Aldrich spiezae; Hashimoto's thyroiditis; allergy; asthma;

Wyral infection; bacterial infection; fungal infection; AIDS; sepsis;

W angina pectoris; crebral ischaemia; congenital heart defect;

R respiratory disorder; neurological disorder; Alzheimer's disease;

W parkinson's disease; inflammation; Crohn's disease; vulnerary;

immunosuppressive; antibacterial; haemostatic; thrombolytic;

maticoagulant; neuroprotective; thyromimetic; antiallergic;

antiachmatic; virucide; fungicide; anti-HIV; nephrotropic; antianginal;

W antiinflammatory; gene; ss.
                       161 GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                      653
 414 AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGTTTA 473
                                                                                                                                                                                                                                                                                                                                  cDNA sequence #164 containing coding region of a human secreted protein.
                                                                                                                                                                            ACD82804 standard; cDNA; 3173 BP
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970S-0040133P.
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970S-0040312P.
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970S-0043312P.
970S-0043314P.
970S-0043318P.
970S-0043568P.
970S-0043568P.
970S-0043568P.
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97US-0043672P.
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11-APR-1997;
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Conservative: Mismatches: Matches: Length:

Indels:

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Claim 4; SEQ ID NO 174; 260pp; English.
97US-0057650P.
97US-005761P.
97US-0057761P.
97US-0068785P.
98WO-US004493.
98US-00149476.
                                     2000US-0190068P
                                                                                                                                                                                                   Duan DR, Hu J, Florer
Brewer LA, Moore PA,
                                                                                                                   HU J.

FLORENCE K A.

OLSEN H S.

FISCHER C L.

EBNER R.

BREWER L A.

MORE P A.

SHORE P A.

SHORE P A.

ILAFLEUR D W.
                                              RUBEN S M.
ROSEN C A.
SOPPET D R.
CARTER K C.
BEDNARIK D P.
ENDRESS G A.
                                                                                                    GREENE J M.
FERRIE A M.
DUAN D R.
                                                                                                                                                                                                                  WPI; 2003-521800/49.
                                                                                         FENG P.
YOUNG P.E.
                                                                                                                                                                  (LIYY/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
                                                                                                                                                                                                                       P-PSDB; AB034537
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08-SEP-1998
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                                               (RUBE/)
(ROSE/)
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(GREE/)
(FERR/)
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(HUJJ/)
(FLOR/)
(OLSE/)
(FISC/)
(EBNE/)
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Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

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100.00%
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                                                                             Percent Similarity:
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Alignment Scores:
Pred. No.:
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                                                                                                                                        Query Match:
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ACD82641-ACD82950 encode human secreted proteins or their fragments.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genes and its encoded prostate cancer antigen proteins, useful for preventing, treating, ameliorating or diagnosing e.g. prostate cancers, thymic hypoplasia, multiple sclerosis, AIDS, angina pectoris or cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  474 ATGGCATCTGTGAACAGCACCTGTAATGTCACACGTGACATGCTCTGTAGAGAAGAAGAA
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                                                                                                                                                                                                                                   TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
                                                                                                                                                                                                                                                                                                                        GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe
                                                                                                                1 LysAspSerGluilePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                   21 AsnileGlnGluProArgGlnValLygileIleAlaTrpThrSerLysThrSerValAla
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3173
1199
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97US-0040162P.
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97US-0056877P

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11-APR-1997;

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22-AUG-1997;
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The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynucleotide fragment of a sequence not given in the specification, or its allelic variant; a polynucleotide fragment of the CDNA sequence; a polynucleotide sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 174; 256pp; English.
              97US-0056879P

97US-0056881P

97US-0056881P

97US-0056884P

97US-0056884P

97US-0056887P

97US-0056888P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RUBEN S M.
SOSPET D R.
CARTER K C.
CARTER K C.
ENDRARIK D P.
ENDRESS G A.
YU G.
NI J.
FENG P.
YOUNG P E.
GREENE J M.
FERRIE A M.
DUAN D R.
UNDAN D R.
UNDAN D R.
CLORENCE K A.
OLSEN H S.
FISCHER C L.
ENERRER C L.
EBBNER R A.
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polypeptide, or its fragment, domain, epitope or species homologue; or a polynucleotide that hybridises under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer. The sequence encodes a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                      413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGACTCCTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGCAAC
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                                                                     Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 3173

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Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z,
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97US-0056636P
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Bednarik DP; Greene JM, Ferrie AM; her CL, Ebner R; Kyaw H;

P-PSDB; ADH74200

Isolated nucleic acid molecules encoding human secreted proteins, useful for preventing, diagnosing and treating disorders associated with aberrant expression and activity.

claim 3; SEQ ID NO 174; 142pp; English

The invention relates to isolated nucleic acid molecules and the human secreted proteins (SPS) they encode. The proteins and nucleic acids may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoletic disorders, candocrine disorders, diseases of the immune system, inflammatory in disorders and many others. Full details of disorders that may be prevented, diagnosed and/or treated by the above methods are given in the specification. The nucleic acid molecules may be used to produce their proteins. The nucleic acid and it's complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the created by the above methods are given in the proteins. The nucleic acids in samples, and therefore which can antigens in the production of antibodies and activity. The anti-SP cantibodies against the proteins and antigonists may also be used to down regulate expression and activity. The anti-SP antibodies may also be used as diagnostic agents for detecting the presence of the proteins in samples (e.g. by represents a human secreted protein cDNA). The present sequence

25-MAR-2004

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                                                                                                                                                                                                                                                                                                         GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
                                                                                                                                                                                                                                                                                                                          MetalaserValasnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu
                                                                                                                                                                           174 AATAICCAAGAACCACGGCAAGTIAAAAICATIGCTIGGACTICIAAAACAICIGTIGCT
                                                                                                              LysAspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                              AsnileGlnGluProArgGlnValLysileIleAlaTrpThrSerLysThrSerValAla
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                                                                                         US-09-882-171-483_COPY_22_220 (1-199) x ADH73891 (1-3173)
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Matches:
Conservative:
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Indels:
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Alignment Scores:
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The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked intantile hypogammaglobulinemia, polyasaccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, Burkitt's hypogammaglobulinemia of infancy, Burkitt's hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's hypersensitivity, rheumatoid arthritis, autoimmune mediated heemolytic anaemia, myasthenia gravis, hypodrenocorticism, glomerulonephritis, or anaemia, myasthenia gravis, hypodrenocorticism, glomerulonephritis, or anaemia, myasthenia gravis, hypodrenocorticism, glomerulonephritis, or anaemia, condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromsome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407
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                                                                                                                                                                                                                                             New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylltis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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                                                                                                                                  Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     750 G; 791 T; 0 U; 0 Other;
                                                                                                                                  Schoenfeld JR,
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Mismatches:
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Matches:
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1039.00
100.00%
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                                                                                                                                Clark H, Dennis K,
               15-SEP-2003; 2003WO-US029097
                                                     16-SEP-2002; 2002US-0411392P
                                                                                                                                                                                          WPI; 2004-329389/30.
                                                                                           (GETH ) GENENTECH
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Best Local Similarity:
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Pred. No.:
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121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140

408 AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGTTTA

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The invention relates to a novel isolated nucleic acid and the PRO
CO polypeptide encoded by it. A protein of the invention has
continical manuatory, antiarthritite, antirhemmatic, immunosuppressive,
costeopathic, antidiabetic, dermaclogical, antipsociatic, antiallergic,
costeopathic, antidiabetic, and respiratory activity. A polymucleotide
contiasthmatic, hepatotropic, and respiratory activity. A polymucleotide
cof the invention may have a use in gene therapy. The PRO polypeptide, its
caponist, antagonist, or antibody that specifically binds to the
caponist invention may have a use in gene therapy. The PRO polypeptide, its
caponist invention may have a use in gene therapy. The PRO polypeptide, its
caponist interactions, recurrenting an immune related disorder such as
constructed in service in tracting an immune related disorder such as
constructed interactions, rheumatorid arthritis, ostecarthritis,
cidopathic inflammatory myopathy, Sjogren's syndrome, systemic
chrombocytopenia, thyroidiseae of the central or peripheral nervous
capstem, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
captem, idiopathic demyelinating polyneuropathy, a hepatobiliary
captem, idiopathic sor autoimmune chronic active hepatitis, primary
chisease, infectious or autoimmune chronic active hepatitis, primary
chisease, infectious or autoimmune chronic active hepatitis,
chistory cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
                        527
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                                                                                                                                                  GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                   AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
                                                                                                                                                                                                                                                           AATTCTGACTCCATCTCTGCCGGCAGCTCTGTGCAGACATCGCGATGGGCTTCCGT 704
LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                                                         AAGAATGTGACATACAATTGGAGTCCCCTGGGAGAGAGGGGTAATGTCCTTCAATCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide encoding cDNA SEQ ID NO:1120.
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                                                                                                                                                                                                                                                                                                                                                                ADP23942 standard; cDNA; 3299 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark H, Schoenfeld J,
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inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.
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Best Local Similarity:
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81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
                                                                                                                                                                                                                                                                                                                                       Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1q22, were the marker is linked to a variant form of the SCZ gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was isolated using the method of the invention as the SCZ gene. This sequence has been previously identified as CD84, GenBank Accession No. NM 008874. CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. The proteins encoded by this sequence may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method of diagnosing susceptibility to schizophrenia in a patient. The method comprises determining the presence or absence of an allele of a linked polymorphic marker in the DNA of the patient. The polymorphic marker in chromosome 1422 and is linked to a gene (SCZ) having a variant form associated with a phenotype of schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
allele; polymorphic marker; chromosome 1q22;
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                                                     Location/Qualifiers
45. .1031
/*tag= a
/product= "SCZ"
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1039.00
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                                                                                                                                                                                                                   21-APR-2000; 2000US-0198873P
                                                                                                                                                                                                                                                                            Brzustowicz LM, Bassett AS;
                                                                                                                                                                                                                                                (RUTF ) UNIV RUTGERS
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Best Local Similarity:
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U; 17 Other;

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BP; 959 A; 802

Sequence 3326

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcome in the manable sarcoma, possibly via gene therapy or vaccine production. The nucleic sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated bNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                   120
                 407
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                                                                                                                                                                                      LyshenValThrTyrAenTrpSerProLeuGlyGluGlyGluGlyAsnValLeuGlnIlePhe 160
                                                                                                                       MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu 140
                                                                                                                                                                                                               GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                                                                                                                                                                        588 cagactecrigaggaccaagagcrigacriaacacgrigacagcccagaacccrigrcagcaac 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                            AAGGGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGTTTA
GAAGACGCAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCCCC
                                                     LysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeu
                                                                                                                                           ATGGCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human soft tissue sarcoma-upregulated DNA - SEQ ID 6219.
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LysAsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe 160
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                                                                                                                                                                                                                                                                                                                                                                                                          MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGCATCTGTGTAACAGCACCTGTAATGTCACACTGACATGCTCTGTAGAGAAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATCTTC
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                                                                                                                                                                  AsnileGinGluProArgGinValLysileIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                               TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                GluaspalaGlyaspTyrLysalaaspIleasnThrGlnAlaaspProTyrThrThr
                                                                                                                                                                                                                                                                                                                                     GAAGACGCAGGAGTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCACC
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                                                                                                                                                                                                                                                                                                                                                                                   AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATTACACAGAGTTTA
                                                                                                                  LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                                                                                TyrGluArg1leHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
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                                                                                           US-09-882-171-483_COPY_22_220 (1-199) x ADQ23399 (1-3326)
        Length:
Matches:
Conservative:
Mismatches:
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                                   Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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The invention relates to a novel isolated polypeptide (NOVX) comprising emature form of any of the 37 amino acid sequences fully defined in the pecification. A polypeptide of the invention has antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, anorectic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiarthritic, antinflammatory, dermatological, antiasthmatic, and antilipaemic activity. A polymucheotide of the invention may have a use in gene therapy. The polypeptides, nucleic acid molecules and antibodies
                                                                                                                                                                                                                                                                                                    antiatreriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antibarkinsonian; dermiconvulsant; osteopenhic; antiathritic; antihiflammatory; dermatcological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGRA4; complement factor I precursor; metalloproteinase-15 precursor; MDC3; T-lymphocyte surface antigen Ly-9 precursor; fibroblast growth factor-21; FGF-11; antilentoproteinase 1 precursor; battle polypeptide variant; antilenkoproteinase 1 precursor; lucial protein-like; beta-neoendorphin-dynorphin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
181 AsnSerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMetGlyPheArg
                   1036 AATTCTGACTCCATCTCTGCCCGGCAGCTCTGTGCAGACATGGCAATGGGCTTCCGT
                                                                                                                                                                                                                                                                                           gene; human; antidiabetic; anorectic; cardiant; hypotensive;
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1. .1581
/*tag= a
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10-SEP-2002; 2002US-0410320P.
16-SEP-2002; 2002US-0410320P.
23-SEP-2002; 2002US-0411060P.
23-SEP-2002; 2002US-0412766P.
24-SEP-2002; 2002US-041276F.
25-SEP-2002; 2002US-0412767P.
25-SEP-2002; 2002US-0413342P.
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                                                                                                                                                                                                                                                  Human NOV5b gene SEQ ID NO:49.
                                                                                                                           ADL57104 standard; DNA; 1581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-315567/29.
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                                                                                                                                                                  ADL57104;
                                                                                    RESULT 14
                                                                                                                           The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AsnIleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATATCCAAGAACCACGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATGTAACACCAGGAGACTCAGAACAGCACCCGTAGTTACTGTGACCCCACAGAATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG
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                                                                                                                           otide associated with breast cancer, useful for polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3687. BP; 1073 A; 881 C; 838 G; 874 T; 0 U; 21 Other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                           Novel isolated polypeptide associated with detecting presence of polypeptide in sample
                                                                                                                                                                                                               Disclosure; SEQ ID NO 13255; 36pp; English.
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                                           Wang Y, Steinmann
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      (MILL-) MILLENNIUM PHARM INC
                                                                                WPI; 2003-787014/74.
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Best Local Similarity:
                                           Xu Y,
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                                           Lillie J,
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g ò 127 GCAGAGAAAAGTGTTCTGTACAGCTGGACCCCAAGGGAACCCCATGCTTCTGAGTCCAAT

GluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys ThralaGlnAsnProValSerAsnAsnSerAsp---SerIleSerAlaArgGlnLeuCys

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173

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cc are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases such as metabolic disorders, hainthic, and protozoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neurodegenerative disorders, Alzheimer's (disease, Parkinson's disease, epilepsy, immune disorders, Alzheimer's cathma, and various dyslipidaemias. The nucleic acids and polypeptides casthma, and various dyslipidaemias. The nucleic acids and polypeptides corther modulate or inhibit es, on neurogenesis, cell differentiation, cell proliferation, haematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to Novx substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenemics. The Novx polypeptides of the invention show homology to certain known human proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4 (FGFR4); NOV2a shows homology to fibroblast growth factor-21 (FGFR4); NOV2a shows homology to fibroblast growth factor-21 (FGFR4); NOV3a-91 show homology to antilenbugoroctinase 1 precursor; NOV3a-91 show homology to antilenbugoroctinase 1 colypeptide variant; NOV8a-89 show homology to antilenbugoroctinase 1 colypeptide variant; NOV8a-89 show homology to antilenbugoroctinase 1 colypeptide variant; NOV8a-89 show homology to antilenbugoroctinase 1 colypeptide variant; NOV8a-89 show homology to antilenbugoroctinase 1 colypeptide variant; NOV8a-80 show homology to antilenbugoroctinase 1 colypeptide variant; NOV8a-80 show homology to antilenbugoroctinase 1 colypeptide variant; NOV8a-80 shows homology to blow homology to antilenbugoroctinase 1 colypeptide varian
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ADK98595 standard; cDNA; 1723 BP

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RESULT 15

ADK98595

1581 77 41 70 14 5 Conservative: Mismatches: Indels: Length: Matches: Gaps: 4.73e-29 352.00 58.42% 38.12% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

Sequence 1581 BP; 422 A; 442 C; 397 G; 320 T; 0 U; 0 Other;

US-09-882-171-483_COPY_22_220 (1-199) x ADL57104 (1-1581)

100 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr---Gln 118 GAGGAGGAATTCACCCCTGTTCGTCTATGAGCAGCTGCAGGAGCCCCAAGTCACCATGAAG 366 138 306 82 AACATCTCAGTAGACACAGAGATTGAGAACGTCATCTGGATTGGTCCCAAAAATGCTCTT 141 246 GCTTTCGCACGTCCCAAAGAAAAT------GTAACCATTATGGTCAAAAGC 186 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg 79 66 AgnileGlnGluProArgGlnValLysileIleAlaTrpThrSer---LysThrSerVal 39 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59 AAGGACTICAGCCCCAACAGTGGTGTCCAGGGATCCTAGGGGGTTCCGTGACTCTCCCCTA 81 ctgaatgatgcaggatcctacaaagcccagataaaccaaaggaattttgaagtcacact SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr LysaspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal 367 21 40 142 9 187 80 247 307 119 ò 셤 ò 셤 à g ò 임 ò g ò 원 8 a ò

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The invention relates to a novel isolated immune response associated protein (IRAP) comprising any of 35 fully defined sequences given in the specification. The polypeptide of the invention demonstrates antiatreriosclerotic, cytostatic, neuroprotective, antiparkinsonian, the patotropic, cerebroprotective, antiinflammatory, nootropic and vasotropic activities and may be useful for treating a disease or condition associated with decreased expression or overexpression of functional immune response associated proteins, while the antibody is useful for diagnosing a condition or disease associated with the expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke, Alzheimer's disease, Parkinson's disease and Crohn's disease.

Trithermore, the molecules of the invention may be utilised during gene therapy procedures. The current sequence is that of a human IRAP cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated immune response associated proteins (IRAP) polypeptide and polymucleotide, useful for diagnosing and/or treating disorders with aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SD;
                                                                                                                                immune response associated protein; IRAP; antiarteriosclerotic; cytostatic; neuroprotective; antiparkinsonian; hepatotropic; ecebbroprotective; antiinflammatory; nootropic; vasotropic; arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease; Parkinson's; Crohn's; gene therapy; human; 88; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,, Elliott VS, Hafalia AJA, Richardson
Marquis JP, Chawla NK, Khare R, Becha
                                                                                                 Human immune response associated protein IRAP-23 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5, SEQ ID NO 58; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2002; 2002US-040756IP.
11.SEP-2002; 2002US-0410178P.
13-SEP-2002; 2002US-041057IP.
18-OCT-2002; 2002US-049906P.
25-OCT-2002; 2002US-0421445P.
                                                                                                                                                                                                                                                                                                                                                            26-AUG-2003; 2003WO-US026988
                                                                    (first entry)
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153 GlugiyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThrTyrThrCys 172
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                                                                                                                                                                                                                                                                   100 ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr---Gln 118
                                                                                                                                                                                                                                                                                                                                                                       434 GAGGAGGAATTCACCCTGTCTATGAGCAGCTGCAGGAGCCCCAAGTCACCATGAAG 493
                                                                                                                                                                                                                                                                                                                                                                                                       SerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLys 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 GCTTICGCACGTCCCAAAGAAAT------GTAACCATTATGGTCAAAAGC 313
                                                                                                                                                                            21 AsnijeGlnGluProArgGlnValLysIleIleAlaTrpThrSer---LysThrSerVal 39
                                                                                                                                                                                                                        40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
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U; 0 Other;
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Matches:
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Indels:
Gaps:
  427 G; 354 T; 0
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Sequence 11, Sequence 9, 1

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US-09-149-476-174

Sequence 174, Application US/09149476

Petent No. 6420526

GENERAL INFORMATION:
TITLE OF INFORMATION:
FILE REPERRICE: P2002P1
CURRENT FILING DATE: 1998-03-08

EARLIER APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-03-06

EARLIER PEPLICATION NUMBER: OC/040,162

EARLIER PELING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

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Sequence 557, App
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Sequence 1456, Application US/09949016
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Best Local Similarity:
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Matches:
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EARLIER FILING DATE: 1997-08-22
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US-09-949-016-1456

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petent No. 6812339
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VERYIER, J. Craig et al. |
| APPLICANT: VERYIER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITHER: US/09/949,016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR APPLICATION NUMBER: 60/231,768 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-06 |
| PRIOR FILING DATE: 2000-10-06 |
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| SOCTION OF SEQ ID NOS: 207012 |
| SOCTION OF SEQ ID NOS: 207012 |
| LENGTH 3296 |
| LENGTH 3296
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Sequence 12299, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-41-4

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: Fasted for Windows Version 4.0
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Sequence 13198, Application US/09949016

Sequence 13198, Application US/09949016

Sequence 13198, Application US/09949016

PATELE NO. 6812339

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CLO01307

CORRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755
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ORGANISM: Human
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                                            Sequence 557, Application US/09949016

Facent No. 6812339

GENERAL INFORMATION:
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US-09-949-016-557
                                  US-09-949-016-557
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US-09-227-357-53
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TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: PZO10P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER PILING DATE: 1999-01-08
EARLIER PILING DATE: 1999-07-08
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEMOIN NO 13198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,931
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Patent No. 6342581
GENERAL INFORMATION:
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571.00
100.00%
99.09%
54.96%
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                   US-09-949-016-13198
                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
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8 valAsnGlyIleLeuGlyGluSerValThrPheProValAsnileGlnGluProArgGln 27 28 vallysileilehlaTrpThrSerLysThrSerValAlaTyrValThrProGlyAspSer 47 US-09-882-171-483_COPY_22_220 (1-199) x US-09-227-357-53 (1-1140) Length:
Matches:
Conservative:
Mismatches:
Indels: ò

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Gaps:
                                                                                                                                              1.31e-10
                                                                                                                                                           160.00
43.15%
25.38%
15.40%
    TYPE: nucleic acid
STRANDEDNESS: single
                                                                        CDS
61..975
                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                       NAME/KEY:
LOCATION:
                                                                                                                                Alignment Scores:
                                                                                                    US-08-348-792-5
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US-08-462-738-5
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88 AlaAspIleAsnThrGlnAlaAspProTyrThrThrThrLysArgTyrAsnLeuGlnIle 107
                                                                                                                                                                                    411 GCTCAAGTCAACCTGAGAACATCCCAGATCTCTACCATGCAGCAGTACAATCTATGTGTC 470
                                                                                                                                                                                                                TyrArgArgLeuGlyLys-ProLysileThrGlnSerLeuMetAlaSerValAsnSerTh 127
                                                                                                                                                                                                                                                                                      531 CTGCAGTATGTCCCCTGGTGTGCTCTGTGGAGRAAGGCAGGCATGGATATGACCTACAGGT 590
                                                                                                                                                                                                                                                                                                                                                         591 GCTCTCCCGGGGGGATAGCACTTATACATTCCATGAAGGCCCTGTCCTCAGCACATCCT 650
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                                                                                                                                                                                                                                                                                                                                                                                                     rpSerProLeuGlyGlu------GluGlyAsnValLeuGlnIlePheG 161
                                             67
                                                                                                68 GlyproAsnTyrAsnLeuValileSerAspLeuArgMetGluAspAlaGlyAspTyrLys 87
                                         48 GluThrAlaProValValThrValThrHisArgAsnTyrTyrGluArgIleHisAlaLeu
                                                                                                                                                                                                                                                                      127 rCysAsnValThrLeuThrCysSerValGlu-LysGluGluLysAsnValThrTyrAsnT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: do Vies, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08348792
Patent No. 5576423
GENERAL INFORMATION:
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US-08-348-792-5
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100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 ---GlyGluGluGlyAsnValLeuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
                                                                                                                                                                                                                              295 GIGICICITGAICCAICCGAAGCAGCCCTCCACGITAICTAGGAGAICGCIACAAGITT 354
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                                                                                                                                                                                  LeuGlyGluSerValThrPhePro-------ValAsnIleGlnGluProArg
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Matches:
Conservative:
Mismatches:
Indels:
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151 ---GlyGluGluGlyAsnValleuGlnIlePheGlnThrProGluAspGlnGluLeuThr 169
                                                                                                                      619 CCAGCCAACAGCTCCCTCCTCACCCTCGGCCCCCCAGCATGCTGACAATATC 678
                                                                                                                                                                                                                                                                               Sequence 5, Application US/09199955
; Sequence 5, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:
    APPLICANT: Average, Gregorio
; APPLICANT: Chang, Chia-Chun J.
    APPLICANT: Cocks, Benjamin G.
    APPLICANT: de Vries, Jan E.
    TITLE OF INVENTION: SURFETED GENES ENCODING MANMALIAN CELL
    TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: DNAX Research Institute
    STREET: 901 California Avenue
                                                                                                                                                                                     170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
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50
35
78
34
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ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
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Matches:
Conservative:
Chismatches:
Indels:
Gaps:
                  138 LysGluGluLysAsnValThrTyrAsnTrpSer
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
APPLICATION NUMBER: US 08/461,473
FILING DATE: 02-DEC-1994
ATTOMNO DATE: 02-DEC-1994
ATTOMNO CABENT INCOMENTION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DNAX Research Institute STREET: 901 California Avenue CITY: Palo Alto STATE: California
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
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STRANDEDNESS: single
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MOLECULE TYPE: CDNA
FEATURE:
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                      RESULT 9
US-09-199-955-5
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                                                           COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: DX0436GB
TELECOWMUNICATION INFORMATION:
TELEROMOR: 415-85-9196
TELECOWMUNICATION INFORMATION:
TELEROM: 415-85-9196
TELECOWMUNICATION OF SEQ ID NO: 5:
SEQUENCE CHARACTERESTICS:
LENGTH: 1020 Dase pairs
TYPE: nucleic acid
STARUBEDRESS: single
TYPE: Ulnear
MOLECULE TYPE: CDNA
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Matches:
Conservative:
Mismatches:
Indels:
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901 California Avenue
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160.00
43.15%
25.38%
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LOCATION: 61..975
                      Palo Alto
: California
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Best Local Similarity:
Query Match:
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Pred. No.:
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43.15%
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APPLICATION NUMBER:
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Best Local Similarity:
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US-08-880-875-5
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US-08-348-792-7
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                                                                                                                                                                                                                         ::: |||::: |||35 agcatccacattgtcacaatggcaaaatcactgggagaacagtgtcgagaacaaata 294
                                                                                                                                                                                                                                                                                                                                                  ::: ||| ::: ||| 295 GTGTCTTTGATCCATCGACGTTATCTAGGAGATCGCTACAAGTTT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 TATCTGGAG-------AATCTCACCCTGGGGATACGGGAAAGCAGG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AAGGAGGATGAGGGATGGTACCTTATGACCCTG-------GAGAAAAATGTTTCA 441
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                                                                                                                   175 Tricicialacalaricerecrecicerearararalararaharaharangaearealean 234
                                                                                                                                                                                                                                                                                                                                                                                                                               60 TyrTyrGluArglleHisAlaLeuGlyProAsnTyrAsnLeuValileSerAspLeuArg 79
                                                            ---ValAsnIleGlnGluProArg 26
                                                                                                                                                                                   ---SerVal 39
                                                                                                                                                                                                                                                                                                         40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 MetGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
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Fatent No. 6399065

GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Codag, Chia-Chun J.
APPLICANT: Codag, Benjamin G.
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US-09-882-171-483_COPY_22_220 (1-199) x US-09-199-955-5 (1-1020)
                                                                                                                                                                               27 GlnValLysIleIleAlaTrpThrSerLysThr-------
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ZIP: 94304-1104
ZIP: 94304-1104
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/880,875
                                                      12 LeuGlyGluSerValThrPhePro----
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-JUN-1995
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US-08-880-875-5
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100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 117
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                           DX0436K
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FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX04
TELECPHONICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEPHONE: 415-496-1200
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 1020 base pairs TYPE: nucleic acid STRANDEDNES: single TOPOLOGY: Linear MOLECULE TYPE: CDNA
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441

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138 LysGluGluLysAsnValThrTyrAsnTrpSer-------ProLeu--- 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 CCAGCCAACAGCTCCCACCTCTGTCCCTCGGCCCCCAGCATGCTGACAATATC 686
                                                                                                   --GAGAAAATGTTTCA 449
                                                                                                                                                                                                                        100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr
                                                                                                                                                                                   118 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu
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Sequence 7, Application US/08462738

Sequence 7, Application US/08462738

Sequence 7, Application General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General General
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MEDIUM TYPE: Floppadiable
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,738
FILING DATE: 05-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELLECOMMUNICATION INFORMATION:
   102 AAGGAGGATGAGGATGGTACCTTATGACCCTG--
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901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1079 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
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153..1073
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CITY: Palo Alto
STATE: California
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LOCATION:
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|B3 TIGGGAAGCAAGTGCIGCIGCCCTGACAIAIGAAAGGAIAAAIAAGAGCAIGAACAAA 242
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                                                                                                APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-882-171-483_COPY_22_220 (1-199) x US-08-348-792-7 (1-1079)
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/348,792

FILING DATE: 02-DEC-1994

CLASSIFICATION: 530

ATTONENY/AGENT INFORMATION:

NAME: Ching, Edwin P:

REGISTRATION NUMBER: 34,090

REGISTRATION INFORMATION:

TELEPRAK: 415-495-1200

INFORMATION: 415-495-1200

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENTH: 1079 Dass Pairs
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             Sequence 7, Application US/08348792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.42e-10
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43.15%
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STRANDEDNESS: single
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LOCATION: 153..1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
                                       Patent No. 5576423
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-348-792-7
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Matches:
Conservative:
Mismatches:
Indels:
                                                                   PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/348,792
RILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/POCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-652-9196
     DATA:
R: US/09/199,955
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1079 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160.00
43.15%
25.38%
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     CURRENT APPLICATION DA APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           153..1073
                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
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Query Match:
DB:
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|63 TATCTGGAG------AATCTCACCCTGGGATACGGGAAAGCAGG 401
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Patent No. 6372899
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjadin G.
APPLICANT: Gocks, Benjadin G.
APPLICANT: Goves, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURRACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                  US-09-882-171-483_COPY_22_220 (1-199) x US-08-462-738-7 (1-1079)
1079
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
Length:
Matches:
Conservative:
Mismatches:
                                                                     Indels:
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                160.00
43.15%
25.38%
15.40%
                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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 Pred. No.:
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100 ThrLysArgTyrAsnLeuGln-----IleTyrArgArgLeuGlyLysProLysIleThr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            627 CCAGCCAACAGCTCCCACCTCGTGGCCCTCGGCCCCCAGCATGCTGAAAAATC 686
                                                                                                                                                                363 TATCTGGAG---------AATCTCACCCTGGGGATACGGAAAGCAGG 401
243 AGCATCCACATTGTCGTCACAATGGCAAAATCACTGGAGAACAGTGTCGAGAACAAAATA 302
                                                                           303 GIGICICITGAICCAICCGAAGCAGGCCCTCCACGITAICIAGGAGAICGCIACAAGIIT 362
                                                                                                                                                                                                            80 MetGjuAspAlaGjyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 99
                                                                                                                                                                                                                                                                                                                            450 GTTCAGCGCTTTTGCCTGCAGTTGAGGCTTTATGAGCAGGTCTCCACTCCAGAAATTAAA
                                        40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn
                                                                                                                            60 TyrTyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Cocks, Benjamin G.
APPLICANT: Gek, Benjamin G.
APPLICANT: Gek, Benjamin G.
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
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CURRENT APPLICATION DATA:
RPPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
S30
ATTORNEY AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE:
415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1716 base pairs
TYPE: nucleic acid
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STATE: California
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                                                     170 TyrThrCysThrAlaGlnAsnProValSerAsnAsnSerAspSerIleSer 186
                                                                                                                                                                                                          APPLICANT: Aversa, Gregorio
APPLICANT: Cang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Ge Vries, Jan E.
TITLE OF INVENTION: PURITED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURPACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE DNAK Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-882-171-483_COPY_22_220 (1-199) x US-08-880-875-7 (1-1079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE PORM:

COMPUTER READABLE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compacible

COMPUTER: IBM PC compacible

COMPUTER: APPLICATION DATA:

APPLICATION NUMBER: US/08/880,875

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                            ADDRESS:

STREET: 901 California Avenue
CITYT: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIPICATION: 435
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION UNUBER: US 08/481,777
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-496-1200
                                                                                                                                                         Sequence 7, Application US/08880875
Patent No. 6399065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.42e-10
160.00
43.15$
25.38$
15.40$
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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153..1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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Pred. No.:
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175 TIGGGAAGCAAAGIGCTGCTGCCCTGACAIAIGAAAGGAIAAAAAGAGCAIGAACAAA 234
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235 AGCATCCACATTGTCGTCACAATGGCAAAATCACTGGAGAACAGTGTCGAGAACAAAATA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 GlnSerLeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGlu 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  502 GITITAAACAAGACCCAGGAGAACGGGACCTGCACCTTGATACTGGGCTGCACACTGGAG 561
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                                                                                                                                                                                                                                                                                                                                     27 GlnValLysilelleAlaTrpThrSerLysThr-------SerVal 39
                                                                                                                                                                                                                                                                                                                                                                                                   40 AlaTyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsn 59
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                                                                                                                                                                                                                                             US-09-882-171-483_COPY_22_220 (1-199) x US-08-348-792-1 (1-1716)
                                                                                                                                         1716
50
35
78
34
                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                    2.85e-10
160.00
43.15%
25.38%
15.40%
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                           FEATURE:

NAME/KEY: CDS

LOCATION: 61..1065

US-08-348-792-1
                                                                                                                                                    Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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Search completed: February 5, 2005, 11:31:57 Job time : 144.551 Becs

Sequence 3

Sequence

Sequence

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Description

Sequence Sequence

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Sequence Sequence

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Sequence Sequence

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APPLICATION: Practicus, Christopher C. TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF FILE REFERENCE: 7853-244-999
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT APPLICATION NUMBER: US/10/007,303
PRIOR APPLICATION NUMBER: 0S/10/007,303
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PALENTIN Version 3.1
                                                 US-10-436-523-29

US-10-68-523-29

US-09-802-391-174

US-09-882-171-174

US-09-882-171-174

US-10-164-861-1174

US-10-198-846-13255

US-10-198-846-13255

US-10-198-846-13255

US-10-198-846-13255

US-10-328-538-1

US-10-328-538-1

US-10-436-523-84

US-10-436-523-93

US-10-436-523-93

US-10-436-523-94

US-10-264-237-216

US-10-264-237-216

US-10-264-237-216

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US-10-264-237-216

US-10-265-144-9

US-10-245-143-75

US-10-245-143-75

US-10-245-143-75

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US-10-238-283-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-436-523-29
'Sequence 29, Application US/10436523
', Sequence 29, Application No. US/20030180888A1
', Publication No. US/2003018088A1
', GENERAL INFORMATION:
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16
16
                 DB
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11139
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Query
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LENGTH: 1040
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-MODEL=frame+ p2n. model -DEV=xlh
-MODEL=frame+ p2n. model -DEV=xlh
-Q=/Cgn2 1/USPG ppcol/US09882171/runat_04022005 114005_26092/app_query.fasta_1.910
-Q=/Cgn2 1/USPG spool/US09882171/runat_04022005 114005_26092/app_query.fasta_1.910
-DB=Published Applications NA -QFMT=fastap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bite -STRAT=1 - END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OOTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=S509882171 @CGN 1 1 582 @runat 04022005 114005_26092
-NCPU-6 -ICPU=3 -NO MMAP -LARGEQUERY -NGG $200R5=0 - WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOTT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                               Pebruary 5, 2005, 09:29:36 ; Search time 423.629 Seconds
(without alignments)
2703.765 Million cell updates/sec
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                                                                                                                                                                                                                                  1 KDSEIFTVNGILGESVTFPV......NNSDSISARQLCADIAMGFR 199
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                             8627612
   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                           nucleic search, using frame_plus_p2n model
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1039
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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Sequence Sequence Sequence

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TYPE: DNA ORGANISM: Homo sapiens

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                                                                                                                                                                                                                                                                    193 AATATCCAAGAACCACGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGGCT
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; Publication No. US20030049618A1
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFRENCE: P2002P2
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SEQ ID NO 174
; LENGTH: 3173
                                                                                                                                                        US-09-882-171-483_COPY_22_220 (1-199) x US-10-723-860-1885 (1-1067)
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Mismatches:
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ORGANISM: Homo sapiens
FRATURE:
LOCATION: (3119)
OTHER INFORMATION: n equals a,t,g, or c
                                                           1039.00
100.00%
100.00%
                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   JS-10-723-860-1885
                                Alignment Scores:
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Publication No. US20040253606A1

Publication No. US20040253606A1

GENERAL INFORMATION:

APPLICANT: Aliz, Natasha

APPLICANT: Ginsburg, Wendy M.

APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

CURRENT APPLICATION NUMBER: US/10/723,860

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: PatentIn Version 3.2

SEQ ID NO 1885

LENGTH: 1067
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R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,569

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R APPLICATION NUMBER: 60/047,503

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R APPLICATION NUMBER: 60/047,581

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R R PILING DATE: 1997-05-23

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NR APPLICATION NUMBER: 60/047,601

NR FILING DATE: 1997-05-23

NR APPLICATION NUMBER: 60/043,580

NR FILING DATE: 1997-04-11

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NR APPLICATION NUMBER: 60/043,568

NR FILING DATE: 1997-04-11
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R APPLICATION NUMBER: 60/047,633
R PILING DATE: 1997-05-23
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R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/040,334
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APPLICATION NUMBER: 60/043,669
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Fublication No. US2003017585841
GENERAL INFORMATION:
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-16
PRIOR PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR PRIOR FILING DATE: 1998-09-08
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RESULT 6
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i Sequence 6219, Application US/10723860
i Publication No. US20040253606A1
i Sequence 6219, Application US/20040253606A1
i Publication No. US20040253606A1
i GENERAL INFORMATION:
APPLICANT: Aziz, Matsaha
i APPLICANT: Zlotnik, Albert
i TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
i TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
i TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
i TITLE OF INVENTION NUMBER: US/10/723,860
CURRENT APPLICATION NUMBER: 60/429,739
PRIOR PELING DATE: 2002-11-26
i NUMBER OF SEQ ID NOS: 8393
i SOFTWARE: PatentIn version 3.2
i SEQ ID NO 6219
i LENGTH: 3326
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NAME/KEY: misc feature
LOCATION: (2531)..(2547)
OTHER INFORMATION: n is
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ORGANISM: Homo Bapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 TATGTAACACCAGGAGACTCAGAACAGCACCGGTAGTTACTGTGGCCCACAGAATTAT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                  141 LysasnValThrTyrAsnTrpSerProLeuGlyGluGlyGlyGlydsnValLeuGlnIlePhe 160
                                                                                    GlnThrProGluAspGlnGluLeuThrTyrThrCysThrAlaGlnAsnProValSerAsn 180
                                                                                                                                            TyrValThrProGlyAepSerGluThrAlaProValValThrValThrHisArgAsnTyr
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         MetalaSerValasnSerThrCysAsnValThrLeuThrCysSerValGluLysGluGlu
                          x US-10-164-861-174 (1-3173)
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US/09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 174
LENGTH: 3173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3119)
OTHER INFORMATION: n equals a,t,g,
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US-10-164-861-174
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NAME/KEY: SITE
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US-10-164-861-174
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                    556 AATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCT 615
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                                                                                                                                                 616 TATGTAACACCCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCCACAGAAATTAT
                                                                                                                                                                                                                   61 TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
                                                                                                                                                                                                                                                                      676 TATGAACGGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATG
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                                                                                      41 TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7500099CB1
US-10-471-449-20
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| Publication No. US2003009974A1
| GENERAL INFORMATION:
| APPLICANT: Lillie, James
| APPLICANT: Ku, Yongyao
| APPLICANT: Wang, Youzhen
| APPLICANT: Wang, Youzhen
| APPLICANT: Wang, Youzhen
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: THERAPY OF BREAST CANCER
| TITLE OF INVENTION: WINDER: US/10/198,846
| CURRENT APPLICATION NUMBER: 60/306,220
| PRIOR APPLICATION NUMBER: 60/306,220
| PRIOR PRIOR DATE: 2001-07-18
| SOFTWARE: FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREES
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LOCATION: 1, 2, 3669, 3670, 3671, 3672, 3673, 3674, 3675, 3676,
LOCATION: 3678, 3679, 3680, 3681, 3682, 3683, 3684, 3685, 3686,
OTHER INFORMATION: n = A,T,C or G
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LENGTH: 3687
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                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
TYPE: DNA
ORGANISM: Homo
                   US-09-860-836B-12
                                           Alignment Scores:
Pred. No.:
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Publication No. US20030054002A1

GENERAL INFORMATION:

APPLICANT: WAKELAND, WARD

APPLICANT: WARELAND, WARD

TITLE OF INVENTION: ISOLATION OF GENES WITHIN SLE-1B THAT MEDIATE A BREAK

TITLE OF INVENTION: IN IMMUNE TOLERANCE

FILE REFERENCE: UTSD:722US

CURRENT APPLICATION NUMBER: US/09/860,836B

CURRENT APPLICATION NUMBER: 60/204,963

PRIOR APPLICATION NUMBER: 60/204,963

PRIOR FILING DATE: 2000-09-21

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12

LENGTH: 2286
                                                                                                                                                                                                                                                             ThrLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThr---Gln 118
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          Length:
Matches:
Conservative:
Mismatches:
Indels:
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          5.25e-35
352.00
58.42%
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33.88%
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                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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   Alignment Scores:
Pred. No.:
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; Publication No. US20040109862A1
; GENERAL INFORMATION:
   APPLICANT: Enterage, Peter
; TITLE OF INVENTION: Methods of therapy and diagnosis using targeting of control of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of the targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets of targets o
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2286
77
41
70
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       Length:
Matches:
Conservative:
Mismatches:
Indels:
              7.22e-35
352.00
58.42%
38.12%
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397 CTGAATGATGCAGGATCCTACAAAGCCCAGATAAACCAAAGGAATTTTGAAGTCACCT 456
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| AACATCTCAGTAGACACAGAGATTGAGAACGTCATCTGGATTGGTCCCAAAAATGCTCTT 291
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Publication No. US20030180888A1
GENERAL INFORMATION:
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES;
FILE REPERENCE: 7583-244-99
CURRENT APPLICATION NUMBER: US/10/436,523
CURRENT FILING DATE: 2003-05-12
FRIOR PILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/706,167
                                                                                                       2448
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Matches:
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           LENGTH: 2448
TYPE: DNA
ORGANISM: Homo s
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US-10-228-538-1
US-10-228-538-1
Sequence 1, Application US/10328538
Sequence 1, Deplication No. US20040109863A1
GENERAL INFORMATION:
APPLICANT: Emtage, Peter
TITLE OF INVENTION: that express Ly-9
TITLE OF INVENTION: that express Ly-9
CURRENT APPLICATION NUMBER: US/10/328,538
CURRENT FILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 2
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SOFTWARE: Patentin
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Publication No. US20030180888A1
GENERAL INFORMATION:
APPLICANT: Fraser, Christopher C.
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF
FILE REFERENCE: 7853-244-999
CURRENT FILING DATE: 2003-05-12
PRIOR FILING DATE: 2003-05-12
PRIOR PILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/706,167
PRIOR FILING DATE: 2000-11-03
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Matches:
Conservative:
Mismatches:
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                NUMBER OF SEQ ID NOS: 100
SOFWARE: Patentin version 3.1
SEQ ID NO 84
LENGTH: 652
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332.00
58.56%
38.12%
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      PRIOR FILING DATE: 2000-11-03
                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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148 GTTGAGAACATCATCTGGCTCCTCTGCCACTGTGGTGCCAGGGAAAGAG 207
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Sequence 75, Application US/10436523;
Publication No. US2003018088A1
GENERAL INFORMATION:
APPLICANT: FRASEr, Christopher C.
TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF;
FILE REFERENCE: 7853-244-999;
CURRENT APPLICATION NUMBER: US/10/007,303;
PRIOR APPLICATION NUMBER: US/10/007,303;
PRIOR PLING DATE: 2001-111-20;
PRIOR PLING DATE: 2001-11-03;
NUMBER OF SEQ ID NOS: 100
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Mismatches:
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                                                            TYPE: DNA
ORGANISM: Homo sapiens
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sapiens

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; SEQ ID NO 93
; LENGTH: 870
; TYPE: DNA
; ORGANISM: HOMO 8:
US-10-436-523-93
                                                                     Alignment Scores:
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US-10-436-523-93
i Sequence 99, Application US/10436523
j Publication No. US20030180888A1
j GENERAL INFORMATION:
i APPLICANT: Fraser, Christopher C.
j TILLE REFERENCE: 7853-244-999
c CURENT APPLICATION NUMBER: US/10/436,523
cURRENT FILING DATE: 2003-05-12
j PRIOR APPLICATION NUMBER: US/10/007,303
j PRIOR FILING DATE: 2001-11-20
j PRIOR FILING DATE: 2000-11-03
j NUMBER OF SEQ ID NOS: 100
j SOFTWARE: Patentin version 3.1
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Mismatches:
Indels:
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Matches:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 870
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Best Local Similarity:
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628 AGT 630
                                ; TYPE: DNA
; ORGANISM: HOMO
US-10-436-523-75
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Pred. No.:
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                                                                                                                                                                                                                                                        28 ValLysileileAlaTrpThrSerLysThrSerValAlaTyrValThrProGlyAspSer 47
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870
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                                    Conservative:
Mismatches:
Indels:
  Length:
Matches:
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Job time : 427.629 secs
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Query Match:
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CD466225 LeukoN2_2
AK088815 Mus muscu
BE449128 ut52609.y
CN793369 4128380 B
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.

1 (Dases 1 to 987)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
1. 987
UI-H-BIO-
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Homo sapiens CD84 gene, VIRTUAL TRANSCRIPT, partial sequence.
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AK087345 B
BY181022
                                                 BU027996 AG090451 BM0827010 CK772231 BY724459 BY724459 BY724459 BY724459 BY724459 BY322555 CK590858 BW328160 AY413809 AC61522 AA463565 BY49229 BI839154
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BM09070
CK772231
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AUTHORS
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-FGAPEXT=7 -YGAPPOP=10 -YGAPEXT=0.5 -PGAPOP=6
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                                                                                             February 5, 2005, 03:27:31; Search time 2623.94 Seconds (without alignments) 2886.805 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                   frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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925-6813.**

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L. Science 302 (5652), 1960-1963 (2003)

Science 302 (5652), 1960-1963 (2003)

E. Chases I to 987)

S. Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission

L. Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Matches:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 987)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysAsnValThrTyrAsnTrpSerProLeuGlyGluGlyAsnValLeuGlnIlePhe
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Mismatches:
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Matches:
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                                         <1. .. > 987
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AY408982.1 GI:39764950
GSS.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

DEFINITION

CV023928

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BG106937 1074 bp mRNA linear EST 30-JAN-2001
602291349F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4385965 5',
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Straudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Progration: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Http://image.llnl.gov
Plate: LLAM1006s row: b column: 14
High quality sequence stop: 638.
High quality sequence stop: 638.
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/lab_host="Ph108 [phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                  TyrvalThrProGlyAspSerGluThrAlaProvalvalThrValThrHisArgAsnTyr
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Homo sapiens
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/wol_type="mRNA"
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Donor vector: Reference: MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"
                                                                                                                                                                                                                                                                         Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 608)

1. (bases 1 to 608)

1. Salaj, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Contact: Vidal M. Marc Vidal Laboratory Dana Farber Cancer Institute

1. Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc Vidaledfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction Using an MGC full-length cDNA as template DNA and ORF specific primers
                                                                                                           CV023928 608 bp mRNA linear EST 20-AUG-2004 1001 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC020063, mRNA sequence.
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  FORWARD: ATGGCTCAGCACCTA
BACKWARD: TAGATCACAATTTCATAGCTTGAAGT
Insert Length: 608 Std Error: 55.00
Plate: 11032 row: 11 column: E
Seg primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
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High quality sequence stop: 607
POLYA=No.
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Homo sapiens
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535 bp mRNA linear EST 10-JAN-2001
PMO-CT0547-091000-001-a04 CT0547 Homo sapiens cDNA, mRNA sequence.
BF754299
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Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mzushina-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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                                                                                                                                                                                          /cell_type="macrophage"
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Mismatches:
Indels:
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                                                                                                                                                     /mol_type="mRNA"
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/clone="MPE08190"
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                  80
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      Site 2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                       LysargTyrasnLeuglnIleTyrargargLeuglyLysProLysIleThrglnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysasnvalThrTyrasnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATATCCAAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTTTGCT
                                                                                                                                                                                                                                                                                   TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                  354 GCAGACGCAGGAGACTACAAAGCAGACAGACATAAATACACAGGCTGATCCCTACACCACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                        414 AAGCGCTACAAACTGCAAATCTATCGTCGGCCTTGGGAAACCAAAAATTACACAGAGTTTA
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                                                                                                                                                                                                                                         AsnileGinGluProArgGinValLysileIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                                                                                                                                                                   TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
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186
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4
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                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                       US-09-882-171-483_COPY_22_220 (1-199)
                                                                                        3.51e-103
930.50
93.56%
92.08%
89.56%
                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bavkaryota; Bukaryota; Bukaryota; Bukaryota; Bovidae; Bovinae; Bos.

Bovinae; Bos.

E. I (bases 1 to 739)

Smith, T.P. L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries A. Unpublished (2003)

Contact: Smith TPL
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USDA, ARS, US Wast Animal Research Center
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                                                                                                                                                                                                    140
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                                                 397
                                                                                                                            22 IleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAlaTyr 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Marc 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibrary made with RNA pooled from multiple tIssues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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                                                                                                  rLysArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLe
tGluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrTh
                               120 uMetalaSerValAenSerThrCyBAenValThrLeuThrCySSerValGluLysGluG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB467388 733 bp mRNA linear 733 bp mRNA sequence. CB467388.1 GI:29273773
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/organism="Bos taurus"
/mol type="mRNA"
/db_xref="taxon:9913"
/tisuue_type="pooled"
/lab_host="DH108"
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Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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CB467388
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| forganism="Homo sapiens" |
| mol_type="mRNA" |
| mol_type="mRNA" |
| dev_stage="mRNA" |
| dev_stage="Adult" |
| folone lib="cT0547" |
| folone lib="cT0547" |
| folone lib="cT0547" |
| from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUU la vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 535)

1 (bases 1 to 535)

1 (bases 1 to 535)

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carralho,A.F., Matsukuma,A., Baidi,S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., Simpson,D.H., Share,M.J., Soares,F., Brentani,R.R., Reis,L.F., Gouza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922

Raxi: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CTO547-
091000-001-a04&t5=2000-00.09&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence start: 7

High quality sequence stop: 533.
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                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LyshapSerGlullePheThrVal-AsnGlylleLeuGlyGluSerValThrPheProVa
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Mismatches:
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98.63%
                    sapiens (human)
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PUBMED
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BP159730 all-length enriched swine cDNA library, adult thymus Sus scroofs cDNA clone THY010074A04 5', mRNA sequence.
BP159730.1 GI:40409203
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EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing of clones derived from oligo-capped cDNA library
                                                                                                                                                                                                                                                      TATGTAACACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTAT
                                                                                                                              476 ATGGCATCTGTGAACAGCACCTGTAATGTCACACTGACATGCTCTGTAANAGAAGAAGA
                                                                                                                                                               AsnileGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAla
                                                                                                                                                                                               177 AATATCCAAGAACCACGCCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCT
                                                                                                                                                                                                                                  TyrValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr
                                                                                                                                                                                                                                                                                                                                                                             GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr
                                                                                                                                                                                                                                                                                                                                                                                                  357 GAAGACGCANGAGACTACATAGCAGACATAAATACACAGGCTGATCCCTACACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 AAGCGCTACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAATT-ACACAGAGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 MetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerVal-GluLysGluGl
                                                                                          LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
                                                                                                                                                                                                                                                                                                        TyrGluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 uLysAsnValThrTyrAsn-TrpSerProLeuGlyGluGlu 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536 AAAGAATGTGACATACCATTTGGAGGCCCCCTGGGCAGAAG 576
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                                                     (1-582)
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 Indels:
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                                                     US-09-882-171-483_COPY_22_220 (1-199)
   67.08%
5
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BP159730
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                                                                                                                            81
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous Block structure in the promoter regions Contact: Yutaka Suzuki
Department of Virology
                                                       61
456 ACATCTGTGAACAGCACCTGTAATGTCACACTGATGTGTGTCTCTGTGGATAAAGAAGAAAAG
                                                                                                                      GluArgIleHisAlaLeuGlyProAsnTyrAsnLeuValIleSerAspLeuArgMetGlu
                                                                                                                                                                                                                                                                                      396 TCCTACAACCTTCAAGTCTATCGTCTTGAGAAGCCAAAAATTACTCAGAGTTTCGTG
                                                                                                                                                                                                                                                                                                                                      122 AlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluiysGluGluLys
                                                                                                                                                                                                                                                                                                                                                                                                             142 AsnValThrTyrAsnTrpSerProLeuGlyGluGluGlyAsnValLeuGlnIlePheGln
                                                                                                                                                                                                                                                                                                                                                                                                                                         516 AATGTGACATACAGTTGGAGTCCACGAAGGGAAAGAGGCCAATGTCCTTCAAATCTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 ACCCTGACAACCAAGGAGAGTTACACGTGTACAGCGTGGAACCCTGTCAGCAAT
                                                   ValThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyrTyr
                                                                                                                                                                                                                                336 GACTCAGGGATCTACAAAGCCGACATAAATGTAGAGACCTCTAAAGTGACGACCACGG
                                                                                                                                                                                                                                                                   102 ArgTyrAsnLeuGlnIleTyrArgArgLeuGlyLysProLysIleThrGlnSerLeuMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 SerAspSerIleSerAlaArgGlnLeuCysAlaAspIleAlaMet 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          636 TCTGACTCCATCTCTGCCCAGCAGCTCTGTGCAGACATCACAATG
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Matches:
Conservative:
Mismatches:
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/db_xref="taxon:9606"
/clone="MPE07792"
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697.00
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92.26%
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Homo sapiens
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Best Local Similarity:
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                                            Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: N.C. GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AsnGlyIleLeuGlyGluSerValThrPheProValAsnIleGlnGluProArgGlnVal
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2709039"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub1"
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                                                                                                                                                                                                                                                           www.bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
POLYA=Yes.
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/organism="Homo sapiens"
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TAG_LIB=NCI_CGAP_Col0
TAG_SEQ=AAAGG"
                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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683.00
100.00%
98.50%
65.74%
                             Tumor Gene Index
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Best Local Similarity:
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                                                      JOURNAL
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            /mol_type="mRNA"
/db_xref="taxon:9823"
/clone="THY010074A04"
/tissue_type="thymus"
/fev stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult thymus"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 402)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 AACACAGACATCACTATAGTAAATGGGATTCTGGGGGGAGTCAGTGACTTTCTCCTTAAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 IleGlnGluProArgGlnValLysIleIleAlaTrpThrSerLysThrSerValAlaTyr 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProValAsn 21
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UI-H-BIO-aah-a-08-0-UI.s1 NCI_CGAP_Subl Homo sapiens cDNA clone IMAGE:2709039 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuMetAlaSerValAsnSerThrCysAsnValThrLeuThrCysSerValGluLysGlu
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||| ||||||:::||| ||| |||
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Matches:
Conservative:
Mismatches:
Indels:
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Homo sapiens
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690.00
83.00%
68.00%
66.41%
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Mus musculus CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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222 ccgaactacaatctggtcattagcgatctgaggatggaagacgcaggagctacaaagca 163
                                                                                                                                                                              89 AspileAsnThrGlnAlaAspProTyrThrThrThrLysArgTyrAsnLeuGlnIleTyr 108
                                                                                                                                                                                                                                       ArgArgLeuGlyLysProLysIleThrGlnSerLeuWetAlaSerValAsnSerThrCys 128
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Sheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submitseion
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                          282 ACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTAGGT
                                                                                                                     ProAsnTyrAsnLeuValIleSerAspLeuArgMetGluAspAlaGlyAspTyrLysAla
                                                                                                                                                                                                 162 GACATAAATACACAGGCTGATCCCTACACCACCACCAGGGCTACAAACCTGCAAATCTAT
                                                         ThralaProValValThrValThrHisArgAsnTyrTyrGluArg1leHisAlaLeuGly
                                                                                                                                                                                                                                                                   102 CGTCGGCTTGGGAAACCAAAATTACACAGAGTTTAATGGCATCTGTGAACAGCACCTGT
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Matches:
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="CD84"
/locus_tag="HCM3405"
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Buacki,H., Yamanaka,I.,

Kiyoswa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schrimi,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Brad,D., Brusic,V.,

Chothia,C., Corbani,L.E., Cousins,S., Gaasterland,T.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kawaji,H., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Okido,E., Ringwald,M.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                               GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThrThr
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LysAspSerGluIlePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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                                                                                                  LysAspSerGlullePheThrValAsnGlyIleLeuGlyGluSerValThrPheProVal
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Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Watlandse, Y., Wang, E., Watenabe, Y., Wang, L., Wang, B., Wang, M., Yang, L., Yang, L., Yang, L., Yang, L., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

I. Malvie 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Fire Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216 Email: genome-resegner.riken.jp, URL:http://genome.gsc.riken.jp/Adachi,J., Alzawa, K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Haysashida,K., Hirozane,T., Houri,F., Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Yoya,S., Miyazaki,A., Murata,M., Nakamura,M., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shitaki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsh,T., Tagami,M., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lorect submarsation
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for trapper-selected cDNAs to prepare Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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/clone_lib="RIKBM full-length enriched, NOD-derived CD11c
+ve dendritic cells"
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Query Match: DB:

Pred. No.:

ORIGIN

FEATURES

120

378

100

80

MEDLINE PUBMED JOURNAL

COMMENT

TITLE

207

Euteleostomi;

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/lab_host="maked (pool of 40 RNAs)"
/clonellb="NIH MGC 126"
/note="Vector: pDNH MGC 126"
/note="Vector: pDNH MGC 126"
/note="Tector: pDNH MGC 126"
/note="Tector: pDNH MGC 126"
/note="Tector: pDNH MGC 126"
/note="Tector: pDNH MGC 126"
/site 2: Sfil (ggccgcctcggc); Double-stranded CDNA was prepared from a pool of 40 cell line polya+ RNAs (bladder 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%); 5' and 3' adaptors were used in cloning as follows:
// ATTCTAGAGGCCGAGAGTGGCCATTAGGGCCGAGTTGGT(30)NN-3'. Full-length enrished library was constructed using the Clontech creator SWART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH MGC 127 and NIH MGC 128). Library created in the laboratory of T. library."
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                                                                        E (Bases 1 to 466)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2903 row: m column: 14
High quality sequence stop: 437.
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                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Conservative:
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AGENCOURT 10434334 NIH MGC 126 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 TTTATAAAACCAGGAGTCAATAAAGCTGAA-----GTTACCATAACCCAGGGCACTTAT 230
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                                                                                                           /tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-882-171-483_COPY_22_220 (1-199)
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597.50
77.84%
61.34%
57.51%
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Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Fsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeseggsc.riken.go.jp, Wit:http://hgp.gsc.riken.go.jp/,
Tel:gl-45-503-9111, Fax:81-45-503-9170)
Telses are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS 03-NOV-2001
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331 GAAGACGCAGGAGACTACAAAGCAGACATACACAGGCTGATCCCTACACCACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrvalThrProGlyAspSerGluThrAlaProValValThrValThrHisArgAsnTyr 60
                                                                                                                                           AGO90451 677 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-090A06.F, genomic survey sequence.
AGO90451
                                                                                                                                                                                                                                            Pan troglodytes (chimpanzee)
pan troglodytes
Bukaryota / Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                               Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D.; Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
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Pred. No.:
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JOURNAL
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81 GluAspAlaGlyAspTyrLysAlaAspIleAsnThrGlnAlaAspProTyrThrThr 100
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8
                          61 TyrGluArg1leHisAlaLeuGlyProAsnTyrAsnLeuVal1leSerAspLeuArgMet
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AF101030 Homo sapi AC012471 Homo sapi CQ431481 Sequence BD2477970 S' ESTE f CQ771933 Sequence AC090143 Homo sapi AF101031 Homo sapi AF101031 Homo sapi AC091523 Mus muscu CQ472630 Sequence AC091523 Mus muscu CQ472630 Sequence AC095815 Rattus no AC095815 Rattus no AC095815 Rattus no AC0326815 Homo sapi AC01428 Human DNA AL831787 Homo sapi AC068311 Homo sapi AC068311 Homo sapi AC068311 Homo sapi AC068315 Homo sapi AC068315 Homo sapi AC068316 Homo sapi

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unidentified
unclassified.

El (Dases I to 3173)

E Loben, S.M., Rosen, C.A., Fischer, C.L., Soppet, D.R., Carter, K.C.,

Bednarik, D.P., Endress, G.A., Yu, G.L., N, J., Feng, P., Young, P.E.,

Greene, J.M., Ferrie, A.M., Duan, R., Hu, J.S., Florence, K.A.,

Olsen, H.S., Ebner, R., Brewer, L.A., Moore, P.A., Shi, Y.,

Lafleur, D.W., Li, Y., Zeng, Z. and Kyaw, H.

186 human secreted proteins

L Patent JP 2002510192-A 173 02-APR-2002;

HUMAN GENONE SCIENCES INC

PN JP 2002510192-A/173

PP 02-APR-2002

PF 06-MAR-1997 US 60/040162,07-MAR-1997 US 60/040161 PR

07-MAR-1997 US 60/040162,07-MAR-1997 US 60/040163 PR

07-MAR-1997 US 60/04036,07-MAR-1997 US 60/040163 PR

N RUBENS, CRAIG A ROSEN, CARRIE L FISCHER, DANIEL R SOPPET, PI

KENNETH C CARTER, DANIEL P BEDNARIK, GREGORY

A ENDRESS, GUO LIANG

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Topology: Linear;
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/product="MAX.3 cell surface antigen"
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    CTCTCCAGATGCACCATGCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCCCAG 2760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andreesen, R., Bross, K.J., Osterholz, J. and Emmrich, F. Human macrophage maturation and heterogeneity: analysis with a newly generated set of monoclonal antibodies to differentiation
                                                                                                                                                                                                            CACTGCTGTTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCATCTCATTCAGCCTTAC CACTGCTGTTTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCATCTCTTTGGTCCTTTGTCACTAAAACTCATCTCATTCACCTTAC
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Direct Submission
Submitted (05-FBB-1998) Krause S.W., Hematology, University of
Regensburg, Franz Josef Strauss Allee 11, Regensburg, D 93042,
GERMANY
                                                                                                                              TACCTCTTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA
                                             CCAGATGTGTGCCCCCCACCCCATGTCCATGTCCTTCAATGCCCACCTCAAAAGG
                                                                     CCAGATGTGTGCCCCCCCCCATGTCCATTACATGTCCTTCAATGCCCACCTCAAAAGG
                                                                                                                                                      TACCTCTTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTCA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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cell aurface antigen; glycoprotein; MAX.3 antigen.
Homo sapiens (human)
Homo sapiens
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Homo sapiens mRNA for MAX.3 cell surface antigen.
AJ223324
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Biochem. J. 346 Pt 3, 729-736 (2000)
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/organism="Homo sapiens"

/mol type="mRNN"

/db xref="taxon:9606"

/clone="HDPFF19"

/cell type="dendrite"

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KEYWORDS
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ORGANISM
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AUTHORS
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Db 2941 ACTAATTATTTGTTTTCCTCACTACATGTACATGTGGGAATTACAGATAAACGGAAGCC 3000	3060	Oy 3067 CACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCATNTNTACTA 3126	Oy 3127 AAAATACGAAATTAGCCAGGTGGGGCACACATCTGTAGTCCCAG 3173	3296 bp DNA linear PAT 03-FEB-2004	ITION Sequence 4648 from Patent WO02068579. SION CQ718714 ON CQ718714.1 GI:42279571 RDS	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.	/ers,E.W. prising a majority of ng expression and other uses			; DB 6; Length 3296;	Matches 3153; Conservative 3; Mismatches 3; Indels 0; Gaps 0; 15 CCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGCACCTATGGATC 74	7 CCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGCACCACCTATGGATC 80 75 TTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGCTGGAAAAGACTCAGAAATCTTCACA 134	135 GTGAATGCCIGCAAACCTGGCCGGAAGGAGCTGGAAAAAACTCIGAAAAAAAAAA	127 GIGARIGOGALICIGOGANGAGICAGICACITICCCIGIARAGICCANGAGCAGCAGGAGAT 202, 195 GITAAAATCATTGCTTGGACTTCTTAAAACATCTGTTGCTTATGTAACACCAGGAGACTCA 254	246 314 306	315 GGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGACGCAGGAGACTACAAA 374	307 GGICCGAACTACAATCIGGICATIAGCGAICTCIAGGAIGGGGAGAGGGGAGAGAGGGAAATC 434 375 GCAGACATAAATACACGGCTGATCCCTACACCACCACCAAGCGCTACAACCTGCAAATC 434 577 GCICGAATTAAATACACAGGCTGATCAAACAAACACAAAAAAAA	GCACC 494

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AATCTGGTCATTAGCGATCTGAGGATGGAAGACGCAGGAGACTACAAAGCAGACATAAAT 360
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                            GGGAAACCAAAAATTACACAGAGTTTAATGGCATCTGTGAACAGCACCTGTAATGTCACA
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         GCTTGGACTTCTAAAACATCTGTTGCTTATGTAACACCAGGAGACTCAGAAACAGCACCC
                                                                             GTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTAGGTCCGAACTAC
                                                                                                                                              AATCTGGTCATTAGCGATCTGAGGATGGAAGACGCAGGAGACTACAAAGCAGACATAAAT
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/podom_start=1
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/prodict="CD84 antigen (leukocyte antigen)"
/protein id="AAH20063.1"
/db_xxef="G1:18043043"
/db_xref="LocueID:8832"
/db_xref="LocueID:8832"
/db_xref="LocueID:8832"
/db_xref="MAHHMILLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIO
EPROYKIIAWTSKTSVAYVTPGDSETAPVYTHRRYYER.HALGPRYNIU'SBLRWE
DAGDYKADINTQADPYTTTKRYNLQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKE
ERNYTHNTGLLSVATORTOFTOTEDDELTYTTCADRIVSNROSSISARQLCADIANG
FRITHITGLLSVLAMPFLLVLILSSVFLFRERRRQDASKKTIYTYTMASRNYQPABS
RIYDEILQSKVLLPSKEEPVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIV!"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502686.
Location/Qualifiers
 2 (bases 1 to 3278)
Strausberg,R.
Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                      Sequencing Center
Center code: BCM-HGSC
Center code: BCM-HGSC
Center code: BCM-HGSC
Contact: angeborn.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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                                                                                                                 WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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/gene="CD84"
/note="synonyms: SLAMF5, hCD84, mCD84, LY98"
/db xref="LocusID:8832"
/db xref="MIM:604513"
25. 1011
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/db %ref="taxon:9606"
/clone="MGC:21324 IMAGE:4385965"
/tissue type="Lymph, lymphoma"
/clone_lib="NIH MGC_85"
/lab host="DH108"
/note="Vector: pCMV-SPORT6"
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cive 3; Mismatches
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/codon_start=1
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	Db 2521 GTCAGAAAAATACCTTATGAGGGGCAGGGCTGAAGCTTGAGGATGAAA 2580	Oy 2787 CATTACATGTCCTTCAATGCCCACCTCAAAAGGTACCTCTTCTGTAAAGCTTTCCCTGG 2846	Oy 2967 ACTACATTGTACATGTGGGAATTACAGATAAACGGAAGCCKGCTGGGGTGGTGGCTCACG 3026 Db 2941 ACTACATTGTACATGTGGGAATTACAGATAAACGGAAGCCGGCTGGGGTGTGGCTCACG 3000 Oy 3027 CCTGTAATCCCAACCTTTGGGAGGCCAAGGCAGCGGGTCACGGGTCAGGGTTCG 3001 CTGTAATCCCAACCTTTGGGAGGCCAAGGCAGGCGGATCACCTGAGGTCAGGATTCG 3006 Oy 3001 CCTGTAATCCCAACATGTGAAACCCCATNINTACTAAAAATACGAAATTAGCCAGG 3146 Db 3061 AGATTAGTCTGGCCAACATGGTGAAACCCCATNINTACTAAAAATACGAAATTAGCCAGG 3146 Db 3147 TGTGGTGGCAACATGGTGAAACCCCATNINTACTAAAAATACGAAATTAGCCAGG 3120 Oy 3147 TGTGGTGGCAACATCTGTAAAACCCATCTCTACTAAAAATACGAAATTAGCCAGG 3120 Oy 3121 TGTGGTGGCAACATCTGTAAACCCCATCTCTCTACTAAAAATACGAAATTAGCCAGG 3120 Oy 3121 TGTGGTGGCAACATCTGTAAACCCCATCTCTCTAAAAATACGAAATTAGCCAGG 3120 Db 3121 TGTGGTGGCAACATCTGTAACTCCAGG 3173 Db 3121 TGTGGTGGCCAACATCTGTAACTCCAGG 3173	RESULT 6 AL138930/ LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS RETURNATION HUMAN DNA sequence from clone RP11-528G1 on chromosome 1, complete sequence. AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138930 AL138830 AL13883 AL13883 AUTHORS LOCUS SUDMISSION TITLE JOURNAL SUDMISSION CENTO LSEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CENTO LSA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
1287 CCAAACTTCTTCCCATCATAGCACATGTAGAAAATAATATTTTATGGCACACTGGGATA 1346 [CTGTATCACTCCAAGCAGCAGAAGAAGCAGCATGCCCAGTATTCCCACTCCCTGTATCCCACTCCCTGTATCCCACTCCCTGTATCCCACTCCCTGTATCCCACTCCCTGTATCCCACTCCCTGTATCCCACTCTCCCTGTATCCCACTCTCCCACTCTCCCACTCTCCCACTCTCCCACTCTCCCACTCTCCCACTCTCCCACTCTCCCACTCTCCCACTCTCCCAGCATATCTTTCTCCACACTCTCCACACTCTCCACACTCTCTCCACAATAGAACTGACTTTCTCCACACTTCTCCAGCAACTGCGTATAATCCAACTATCTCCCAGAACTCGGTATAATCCAACTTCTCCAAAATAGAACTTGCAAAAAAAA	2100 2160 2246 2220 2306 2380 2340 2426

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requests: clonerequest@sanger.ac.uk
On Sep 10, 2001 this sequence version replaced gi:15021284.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (1.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one Mi3 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with thair source databases: Em: EMBL: Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORNFEP; Information on the WORNFEP
database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromesome 1. constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/PGP/Chr1
RPII-SSG1 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: TWAPPARMY. This sequence is not the entire insert of clone
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The true left end of clone RPI1-528G1 is at 1 in this sequence. The true left end of clone RPI1-404F10 is at 173387 in this sequence. The true right end of clone RPI1-517F10 is at 82222 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote="Sequence from overlapping clone RP11-517F10 (AL445230). Assembly confirmed by restriction digest."
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/db_xref="taxon:9606"
/chromsone="1"
/clone="RP11-528G1"
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                                                                                               108696 CAAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAAA
                                                                                                                                                                                                                                                                                   1620 GAGCAGAATGTGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108276 GGCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGCTGTGTGGGTCTCTGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1800 TGCAGGGTCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATITICITICIGGCCAAGATITICCTTCTGTATCACTCCAAGCAGCACCTCAGCAGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGCCATGCCCAGTATTCCCCACTCTCCAAAAGGAACTGACCAGCTTATATTTCTCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGGGGAACTGGGTATAATCCAACCATCAAATAGAAGACCTTGCAAGAAGCAGAGTCA
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                                                                                                                                                                                                       ATAATATTTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCA
                                                                                                                                                                                                                                                         TATGACTAGAGGCCTCTTGTGACTGGAGGTAACAACCCTGCCCAGTAACTGTGGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1680 GGCATAACAGGCTTAGTAAGTCCAAACACAGATGACAGTGCTGTGTGGGGTCTCTGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTGTGGCTCTCAGCCATGTAGACACACTCTCCAAATGGAGTGTTGGAAAATGTTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTCCAGAAGGAACTTGGGAGATGATGGTGCAGATGAAACTGGGGTTCATCCAGTT
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                                                                                                                                                       ATAATATTTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGCA
                                                                                                                                                                                                                                                                                                                                                              GGGATCAATATTTTGCACACCTGTAATAGGCCATGGCACCAGCCAAGATGCTCTGCTC
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Direct Submission
Submitted (199-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9231058.
                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 57% of reads
Chemistry: Dye-terminator BT-amersham; 42% of reads
quality: 170939 bases at least Q40
Consensus quality: 172842 bases at least Q30
Consensus quality: 173860 bases at least Q20
Insert size: 175698; sum-of-contigs
Insert size: 182579; 24.9% error; agarose-fp
Quality coverage: 5.06x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130404 130503: contig of 2434 bp in length
130504 130503: gap of 100 bp
130504 133199: contig of 2696 bp in length
13200 133299: gap of 100 bp
13300 176698: contig of 43399 bp in length
12. Location/Qualifiers
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g of 3532 bp in length
f 100 bp
g of 2798 bp in length
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of 18156 bp in length
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clone_end:SP6
vector side:left"
8105. 11636
/note="assembly_fragment:01702
fragment_chain:1"
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                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 bp
                                                                                                                                                                                Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1. .8004
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8104: gap of 1
11636: gap of 1
14534: contig o
14534: contig o
14634: gap of 1
94998: contig o
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gap of 1
contig
gap of 1
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/clone="RP11-77110"
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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                       COMMENT
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                                          .07676 CAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCAATGG 107617
                                                                                                                                                                                                                                                                                                  .07496 TGTCTGCTCTTGTGTAGCTCAGGAGACAATTCCAGCACAGACACTACAGTTAACGCTGAA 107437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107616 CIGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCATCTAGCA 107557
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Homo sapiens chromosome 1 clone RP11-77110 map q21.3-23.1, 11
unordered pieces.
CAAGIATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCAATGGG 2339
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                               107436 CTGCAGCTGCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGGCAGGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2880 ACACTGCTTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCATCTCATTCAGCCTTA
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                                                                                        CTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCATCAGCA
                                                                                                                                                                                2400 CCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTAGAAGATGTGCATAA
                                                                                                                                                                                                                                                                          TGTCTGCTCTTGTGTAGCTCAGGAGACAATTCCAGCACAGACACTACAGTTAACGCTGAA
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AL3559662
HTG; HTGS_PHASE1; HTGS_CANCELLED.
HOWO sapiens (human)
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KEYWORDS
SOURCE
ORGANISM
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78361 AGGAAAATGTACCCTTCGCTTGAGGCAGATGCAGCCCTTCCCCCGAGTGCATGGCTTGGA 7830: 1620 GAGCAGAATGTGGGCTGCATATAAGCACACTCATCCTTTGTCTGGGAATCTTTGTGCAG 1679		1740 GTIGTGGCTCTCAGCCAIGTAGACACACTCTCCAAATGGAGTGTTGGAAAATGTTCTTTC 1799 181 GTIGTGGCTCTCAGCCAIGTAGACACTCTCCCAAATGGAGTGTTGGAAAATGTTCTTTC 7812;	1800 IGCAGGGTCTAGAGACTGCTGGGACACTTTCTTGGAGTGCTACTTCAGAAGCCTTATAG 1859	1860 GATTTTCTTTCTGGCCAAGATTTCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAG 1919 	1920 CAGCCATGCCCAGTATTCCCACTCTCCAAAAGGAACTGACCGGCTTATATTTCTCACACT 1979	1980 TCTGGGGAACTGGGTATAATCCAACCATCAAAATAGAAGCCCTTGCAAGAAGCAGAGTCA 2039 		2100 CCAAAGACTCÁGAGAACTAGAGTTTAAGCTGAGGCAGAGTGCCGCCACCTGGCATGCCC 2159	221	TTCACAACTGAGGAAGATTCATATGATCATTTAAGGAAGTGTTTCCCTTATGG 227		CIGCATITAGGCAGATAAAAAATTAAATCAATGAATCAATCAATCAA	CCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTAGAAGGTGTGTGT	2460 IGTCTGCTCTTGTGTAGGTCAGGAGAATTCCAGCAGAGACTACAGTTAACGCTGAA 2519	401 CTGCAGCTGCAAGTAATAGCATGAACAGTCAGAAAATACCTTATGAGGGGGCAGGGCTG 7	AAGCTGGGCCTTGAAGGATGGATGAATTTGGATAGAGAATGAGGAAGACAGAGGCCTC	281 CAAGTGAGAAAGCATGAAAAATGAGCAGGGGCCTGGATCAGTGGGGTGTATTCAGAGCA 772
da Qy	& g	cy B	S S	S G	දු පු	\$ 6 6	ò a	<i>₹</i> 60	oy Q	Oy GD	රු පු ර	å d	ර් පි	상 음 6	3 A 6	i a ć	Z 43
misc_feature 1173714534 fragment:01924 //note="assembly_fragment:01924 fragment_constructions of the construction of the co		misc_reature 10233: .121400 fragment_chain:2" misc_feature 121509 .123702	/note="assembly fragment:01265 fragment_chain:3" misc_feature 123803. 127869 /note="assembly_fragment:02405	fragment_chain:3" misc_feature 127970. 1319403 fragment_chain:3" fragment_chain:3"	isc_feature 130504. /note="a: isc_feature 133300. /note="a:	ore 2201.2; DB 2; Length 176698; ed. No. 0;	Matches 2203; 960 TTT 20051 #CT	1020 TATGAAATTGTGATCTAGGCTGCACAAATTCTCCCTCTGGAAACTGAGTTACAACC 1	78901 TATGAAATTGTGATCTAGGCTGGCTGGGCTGAAATTCTCCCTCTGGAAACTGAACTGAATTACAACC 7 1080 ACCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATT 1 1080 ACCAATACTAGCTGCTGAATCTTCTCTGCAATCTTACTGGAGAATT 1 1000 ACCAATACTAGCAACTTCTCTGAATCTTCTTCTAATCTGAAGATT 1	TAGCTTG 119	1200 TGCCTAAATGGACAAATGGATGCATACCCTTCCTGAAATGACTCCCTTCTGAATGAA	OY 1260 CAAAGCAGGTTACCTAGTATTCCCCAAACTTCTTCCCATCATGAACATGTAGAAA 1319 Db 78661 CAAAGCAGGTTACCTAGTATAGTTTTCCCAAACTTCTTCCCATGATAGCACATGTAGAAA 78602	1320 ATAATATTTTTATGGCACACTGGGGATAAACAAGCAAGAATTGCTCACTTCTGG 	1380 TATGACTAGAGGCCTCTTGTGACTGGAGGTAACAACCCTGCCCAGTAACTGTGGGAGAAG 14	QY 1440 GGGATCAATATTTTGCACACCTGTAATAGGCCATGGCACCAACCA	Qy 1500 ACAGTCAGTATGTGTGAAGATCCCTGGTGCGTGCCTTCACCACGCATCTTGAGCAAATT 1559 Db 78421 ACAGTCAGTATGTGTGAAGATCCCTGGTGCGTGGCCTTCACCACGATCTTGAGCAAATT 78362	Oy 1560 AGGAAANGTACCCTTCGCTTGAGGCAGATGCAGCCCTTCCCCCGAGTGCATGGA 1619

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173495 TATGAAATTGTGATCTAGGCTGCTGGGCTGAATTCTCCCTCTGGAAACTGAGTTACAAC 173436
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                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
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gap of unknown length
contig of 30526 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 12985 bp in length
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unknown length
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Submitted (28-OCT-1999) Genome Therapeutics Corporation, 100 Beaver
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Homo sapiens chromosome 01 clone RP11-566D7, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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On Aug 24, 2000 this sequence version replaced gi:8569080
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AC012471.7 GI:9887680
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
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Smith, D.R.
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171515 GGAAGCC 3060 GGCGGAT	CAGCCATGCCCAGTATTCCCAGTCTCCCAAAAGGAACTGACCTTATATTTCTCCACTCAGCTTATATTTCTCCACTCACT	è 4
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21	160 CACAAACAGATCACCAGCCAGCTTACACAGGCATTAACTCCTCCAATGAGGAAGAATCA 221.	0 0 0
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22	280 CAACTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCAATGGG 2339 	19
23	340 CTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCATCTAGCA 2 	6 1
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27(00 CCTCTCCAGATGCACCATGCTCACAGTCCCTTGCCTATGTGTGGCAGAGTGTCCA 275	59 1756
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28	O GTACCTCTTCTGTAAAGCTTTCCCTGGTATCAGGAATCAAAATTAATCAGGGATCTTTTC 287	79 1636
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DBFINITION Homo sapiens chromosome 1 clone RP11-575N16 map 1, WORKING DRAFT

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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Context: sequence submissions@genome.wi.mit.edu
Context: sequence Information
Center project name: L8310
                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 1, clone RP11-575N16
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Homo sapiens (human)
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: M3; M77815; 100% of reads Sequencing vector: M3; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 174880 bases at least Q40 Consensus quality: 182150 bases at least Q30 Consensus quality: 185136 bases at least Q20 Insert size: 176000; agarose-fp Insert size: 186457; amm-of-contigs Quality coverage: 4.5 in Q20 bases; sum-of-contigs Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
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Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MaR-1998) Servei d'Immunologia, Hospital Clinic,
Villarroel 170, Marcelona 08036, Spain
Location/Qualifiers

1. .1067 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" 1. .1067

/gene="CD84" 70. .1056 /gene="CD84"

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CAAGTATAATCGGCTAAATCCCAATGAATAGTCCTAGGCTGGACAGGCAATGGG
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/codon_start=1 /product="leukocyte differentiation antigen CD84 isoform CD84c"

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EKNYTYNWSPLGEEGNVLOJ PGYPEDDELTYTCTAQNPVSNNSDSISARQLCADI AMG
PRTHITGLLSVLAMPELLVLILSSVFLFRLFRRRQDASKKTIYTYTMASRAYOPAES
RIYDEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIVI"
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AP054815
AP054815.1 G1:6650105
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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1067)
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

LOCUS DEFINITION RESULT 10 AF054815

us-09-882-171-174.rge

Oy 255 GAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAACGGATACATGCCTTA 	753 Qy 315 794 Db 306	813 Qy 375 GCAGACATAAATACACAGGCTGATCCCTACACCACCAAGGCTACAAATCCTGCAAATC 854 Db 366 GCAGACATAAATACACAGGCTGATCCCTACACCACCACGAGGCTACAACTCGCAAATC 973	435 TATCGTCGGCTTGGGAAACCAAAATTACACGAGTTTAATGGCATCTGTGAACAGCACC 4	GATG	GATG 993 Oy 555 AGTCCCTGGGAGAAGAGGGTAATGTCCTTCAAATCTTCCAGACTCTGAGGACCAAGAGGGATCTTCAAATCTTCCAGACTCTGAGGACCAAGAGGAGAAGAGGGTAATGTCCTTCAAATCTTCCAGACTCCTGAGGACCAAGAGGAGAAGAGGGTAATGTCCTTCAAATCTTCCAGACTCCTGAGGACCAAGAGGAGAAGAAGAGGAGAAAAGATCCTTCAAATCTTCCAGACTCCTGAGGACCAAGAGGAGAAGAAGAAGAAGAAGAAGAAGAAGA	GA1 7103	Oy 675 CGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGTACTCACCACCGGGTTGCTGAGC 734	PAT 12-AUG-2002	Oy 795 TTCAAGAGAAGACAAGATGCTGCCTCAAAGAAAACCATATACACATATATCATGGCTTCA 854	eostomi; Qy 855	915	Qy 975 GGGAAAGCCAGCACACACACACACACACACACACACACA	1040; 0y 1035 TAGGCTGCTGGGCTG 1049	74 RESULT 12 HSU82988 65 LOCUS DEFINITION	TCACA 134 ACCESSION U82988.1 GI:2618739 TCACA 125 KEYWORDS	GCAA,194 :	REFERENCE
CCGTACTCACCACACCCC	cascascrictaracascrictaracascrictaricarcacacacacascristasc	GIGCTGGCTATGTTCTTTCTGCTTGTTCTCATTCTGTCTTCAGTGTTTTTGTTCGTTTTG TTCAAGAGAAGACAAGATGCTGCTCAAAGAAAACCATATACATATATCATGTTCTTCA TTCAAGAAGAAGAAGAAGATGCTGCTCAAAGAAAACCATATACACATATATCATGGTTTCA TTTTTAAGAAGAAGAAGAAGAAAAAAAAAA	814 II.CAAGAGAGAGACAGGCCICCAGAGAGAGAGAGAGAGAGAG	AGGAACACCCAGCCAGCAGCAGCAGCAGCAGAACCAALGAAGAACCAGGAAACACCAGGAACAGAACAGAACAGAACAGAAGA	CCCTCCAAGGAAGAGCCAGTGAACACAGTTTATTCCGAAGTGCAGTTTGCTGATAACGGAAAGGCAAGGCAGTTTGCTGATAACGCCTCGGGACTTCAAGCTATGAAATTGT	994 GGGAAAGCCAGCACACACACAGAAACCICCIGGGACIICAAGCIAIG 1035 TAGGCTGCTGGGCT 1048 	Í 1067	1040 bp DNA linear from Patent EP1223218.	GI:22213881 ns (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1	Cd2000 and cd2001 molecules and uses thereof Patent: EP 1223218-A 29 17-JUL-2002; Millennium Pharmaceuticals, Inc. (US)	11040 Corganism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	DB 6; Length e-295; 1; Indels	CCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGCACCACCATGGATC 	TTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGCTGGAAAAGACTCAGAAATCT 	GTGAATGGGATTCTGGGAGAGTCAGTCACTTTCCCTGTAAATATCCAAGAACCACGGCAA.194 	

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
CTGACTTACACGTGTACAGCCCAGAACCCTGTCAGCAACAATTCTGACTCCATCTCTGCC
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H.sapiens mRNA for leukocyte differentiation antigen CD84.
Y12632
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Direct Submission
Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Submitted (15-APR-1997) A. Gaya, Hospital Clinic, Servei
Immunologia, Villarroel 170, Barcelona 08036, SPAIN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
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70. .1089
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leukocyte differentiation antigen
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Unpublished
2 (bases 1 to 1100)
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Homo sapiens
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AUTHORS
TITLE
JOURNAL
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EPRQVKIIAWTSKTSVAYVTPGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRWE
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EKNYTYNMSPLGEEGNVLQIPGYTPGDELTYTTAQNPVSNNSDSISARQLGADIAMG
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RIYDEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDASKESYEIVI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 GGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGACGCAGGAGACTACAAA 365
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                                                                                            Fundacio Clinic, Villarroel
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/organism="Homo sapiens"
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/chromosome="1"
/map="1q4"
/cell_line="Raji; B cell line"
42. .1028
/note="member of immunoglobulin superfamily"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                       C (bases 1 to 1040)
de la Fuente, M.A., Pizcueta, P. and Engel, P.
Direct Submission
Submitted (21-DEC-1996) Hepatology, Fundacid
170, Barcelona 08036, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            product="leukocyte antigen CD84"
protein_id="AAB84364.1"
db_xref="G1:2618740"
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Pred. No. 6.9e-295;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 1034; Conservative
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This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is part of a collection of human full ORF clones jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.

This CDS has been cloned without stopcodon.

The CDS has been inserted into pDONRZO1 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. AAAAAA GCA GGC TCC ACC (ATG).

The last codon is followed by the 3' att site: GACCCAGCTTTCTT. att The clone is validated by till sequence check.

Compared to the reference sequence NM_003874 (GI:4502666) we found AA exchange(s) at position (first base of changed triplet):

880(pro-ser)

Clone distribution: http://www.rzpd.de/products/orfclones/.
                                                                                                                                                                     CR541847 linear PRI 29-JUN-2004 Homo sapiens full open reading frame cDNA clone RZPDo834H0132D for gene CD84, CD84 antigen (leukocyte antigen); complete cd8, without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RZEPD; KZPDO834H0132D, ORFNO 3790
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDO834H0132D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
994 GTTTATTCCGAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAAGACAGTAAA 1053
                                                                                                                                                                                                                                                                                                                                Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 984)

Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,

Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,

Korn, B., Zuo, D., Hu, Y. and LaBaer, J.

Cloning of human full open reading frames in Gateway (TM) system
entry vector (pDoNR201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone=RRZPDO634H0132D"
/clone lib="Human Pull ORF Clones Gateway(TM) - RZPD"
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/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 984)
Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S., Neubert, P., Ebert, K., Schatten, R., Shen, B., Henze, S., Mar, W., Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
                                      Gateway (TM), complete cds
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/db_xref="taxon:9606"
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CR541847
CR541847.1 GI:49456648
Full ORF shutcle clone, G
Homo sapiens (human)
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/gene="CD84"
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                                                                                                                                             CCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGCACCACCTATGGATC
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    /product="leukocyte differentiation antigen CD84"
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                                                                Length 1100;
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                                                                31.2%; Score 991; DB 9; L. llarity 96.9%; Pred. No. 2.7e-282; Conservative 0; Mismatches 0;
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                                                                                      Best Local Similarity
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Catarrhini, Hominidae, Homo.
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                                                GAAATCCTGCAGTCCAAGGTGCTTCCCTCCAAGGAAGAGTCAGTGAACACAGTTTATTCC
                                                                                                 GAAGTGCAGTTTGCTGATAAGATGGGAAAAGCCAGCACACACGACAGGACAGTAAACCTCCTGGG
       GAAATCCTGCAGTCCAAGGTGCTTCCCTCCAAGGAAGAGCCAGTGAACACAGTTTATTCC
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Palou, E., Sole, J., Pirotto, F. and Gaya, A.
Direct Submission
Submitted (20-MAR-1998) Servei d'Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain
Location/Qualifiers
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/product="leukocyte differentiation antigen CD84
CD84#
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95.3%; Pred. No. 6e-277;
iive 0; Mismatches 0;
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/organism="Homo sapien:
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RIYDBILQSKVLPSKEESVNTVYSEVQFADKMGKASTQDSKPPGTSSYEIVI"
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Aax41382 Human sec	Aax41380 Human sec	Aal15199 Human bre	Acn85220 Breast ca	Aak83192 Human imm	Aak74891 Human imm	Aak67271 Human imm	Aak69231 Human imm	Aak91225 Human dig	Aak91226 Human dig	Aak91227 Human dig	Ada02678 Human TOP	Adb72416 Human TIO	Ade95926 Human TOP	Aak88826 Human dig	Abd32953 Human can		Adg97695 Human can	Adq59374 Human can	Abd32872 Human can	Acn44890 Human gen	Adpl3332 Renal cel	Adol5882 4 synthes	Aba20740 Human ner	Aal36330 Human mus
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ALIGNMENTS

RESULT 1

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; ospitive disorder; schizzophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm. Human secreted protein gene 164 clone HSAWF26. AAV59674 standard; DNA; 3173 BP 97US-0038621P. 97US-0040161P. 97US-0040162P. 97US-0040163P. 97US-0040333P. 98WO-US004493. 97US-0040336P. 97US-0040626P. 97US-0043311P. 97US-0043312P. 97US-0043313P 97US-0043314P 19-JAN-1999 (first entry) WO9839448-A2. Homo sapiens. 06-MAR-1998; 07-MAR-1997; 07-MAR-1997; 07-MAR-1997; 11-SEP-1998. 07-MAR-1997 AAV59674; AAV59674

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This sequence represents a nucleic acid molecule designated Gene 164 from the human cDNA clone HSAWF26 (deposited as clone ATCC 97903 and ATCC 979049) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV5951-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the presence of mutations in the new polynocleotides by determining the presence of mutations in the new polynucleotides, based on which tissues are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for
                                                                                                                                                                                                                       Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
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97US-0056894P.
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P-PSDB; AAW74891.
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                                   AGCTGGGCCTTGAAGGATGGATGAATTTGGATAGAGAATGAGGAAGACAGAGGCCTCC
                                                                                                                         CTCTCCAGATGCACCATGCATGCTCACAGTCCCTTGCCTATGTGTGGCCAGAGTGTCCCAG
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New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or preservative. Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Gr Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

Brewer LA;

Greene JM

The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 CDNA sequences also given in the specification, encoded by one of 309 CDNA sequences also given in the specification. The protein is used in a condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferation conditions in nervous system disorders e.g. cerebral ischaemia, cargiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders conspitualin cell proliferation, to prevent skin aging due to subburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of primary tissues, to regenerate tissues and in chemotaxis. The culture of the preserve the servertive to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was contained in electronic format directly from USPTO at

Sequence 3173 BP; 910 A; 773 C; 712 G; 772 T; 0 U; 6 Other;

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Match 99.9%; Score 3169.4; Local Similarity 100.0%; Pred. No. 0; es 3173; Conservative 0; Mismatches

Query Match 99.9 Best Local Similarity 100. Matches 3173; Conservative

DB 6; Length 3173;

1080 1081 CCAATACTGGCAGGTTCCCTGGATCCAGATCTTCTCTGCCCAACTCTTACTGGGAGATTG 1140 1020 1080 1020 900 780 780 909 900 9 720 360 420 420 480 480 180 caccaddadactcadadacadcacccdragtracrereaccacadaaarrarraaac 300 ATGAAATTGTGATCTAGGCTGCTGGGCTGAATTCTCCCTCTGGAAACTGAGTTACAACCA CTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGCAACAATTCTG AcreearcresecesseserererseasAceareseaaresserreceaacacacaca TTTTGTTCCGTTTGTTCAAGAGAAGACAAGATGCTGCCTCAAAGAAAACCATATACACAT ATATCATGGCTTCAAGGAACACCCAGCCAGCAGAGTCCAGAATCTATGATGAAATCCTGC AGTCCAAGGTGCTTCCCTCCAAGGAAGAGCCAGTGAACACAGTTTATTCCGAAGTGCAGT TTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGGACTTCAAGCT 61 ACCACCTATGGATCTTGCTCCTTTGCCTGCAAACCTGGCCGGAAGCAGCTGGAAAAGACT CACCAGGAGACTCAGAACAGCACCCGTAGTTACTGTGACCCCACAGAAATTATTATGAAC GGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGACG CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCACCAGCGCT ACTCCATCTCTGCCCGGCAGCTCTGTGCAGACATCGCAATGGGCTTCCGTACTCACCACA ACCACCTATGGATCTTGCTCCTTGCAAACCTGGCCGGAAGCAGCTGGAAAAGACT ACAACCTGCAAATCTATCGTCGGCTTGGGAAACCAAAAATTACACAGAGTTTAATGGCAT Acaaccrecaaarcrarcerceecrreesaaaccaaaarracacagagrrraareecar TGACATACAATTGGAGTCCCCTGGGAGAAGAGGGTAATGTCCTTCAAATCTTCCAGACTC CTGAGGACCAAGAGCTGACTTACACGTGTACAGCCCAGAACCCTGTCAGCAACAATTCTG CCGGGTTGCTGAGCGTGCTAGCTTCTTTCTGCTTGTTCTCATTCTGTCTCAGTGT 1 TCGACCCCASGCGTCCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGC AAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCTTATGTAA CAGGAGACTACAAAGCAGACATAAATACACAGGCTGATCCCTACACCACCACCAAGCGCT 961 181 181 361 1021 1021 241 421 661 661 721 781 781 841 901 61 241 301 361 421 481 481 541 541 601 601 721 841 901 961 셤 ð 셤 a 셤 ઠે g ઠે 셤 ઠે 용 ò 셤 g 엄 g ò g ò ò 유 ò ò 셤 ò 8 ò ò 셤 ò 셤 ò ò

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ROSEN C A.
SOPPET D R.
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17-MAR-2000;
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(HUAN/)
Human, secreted protein; hyperproliferative disorder; leukaemia;

Wreast cancer; wound; reproductive disorder; blood-related disorder;

M haemophila; thrombocytopaenia; immunodeficiency; thymic hypoplasia;

W Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;

Graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;

W viral infection; bacterial infection; fungal infection; AIDS; sepsis;

W angina pectoris; cerebral ischaemia; congenital heart defect;

R angina pectoris; cerebral ischaemia; congenital heart defect;

R angina pectoris; carebral ischaemia; congenital heart defect;

R angina pectoris; carebral ischaemia; congenital heart defect;

R angina pectoris; carebral ischaemia; congenital heart defect;

R angina pectoris; carebral ischaemia; congenital heart defect;

R antinachuseny disorder; neurological disorder; Alzheimer's disease;

M municoagulant; neuroprotective; thyromimetic; intiallergic;

M cerebroprotective; cardiant; nootropic; antiaparkinsonian;

M cerebroprotective; cardiant; nootropic; antiparkinsonian;
                         cDNA sequence #164 containing coding region of a human secreted protein.
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9705-0040162P

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                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of novel human secreted proteins and the polymucleotide sequences encoding them. The invention also discloses vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The polypeptide and polymucleotide sequences for the secreted proteins are useful for preventing, treating, ameliocating or diagnosing medical conditions such as hyperproliferative disorders (e.g. leukaemia or breast cancers), wounds, reproductive disorders (e.g. leukaemia or breast cancers), wounds, reproductive thrombocytopaenia), immunodeficiencies (e.g. haemophilia or thrombocytopaenia), immunodeficiencies (e.g. graft-versus-host disease, thymic hypoplasia), autoimmune disorders (e.g. graft-versus-host disease, wultiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma), viral or bacterial or fungal infections (e.g. graft-versus-host disease).

C disorders (e.g. kidney failure), cardiovascular disorders (e.g. asthma), cardiovascular disorders (e.g. angina pectoris, cerbral ischaemia or congenital heart defects), respiratory calsorders (e.g. widney failure), cardiovascular disorders (e.g. angina pectoris, cerbral ischaemia or congenital heart defects), respiratory calsorders (e.g. disorders), and inflammations (e.g. Crohn's disease). The polymucleotide or polypeptide may also be used as vaccine adjuvants.

C ADD82641ACD82950 encode human secreted proteins or their fragments.

C Specification, but was obtained in electronic format directly from the
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Greene JM, Fer:
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(P, Young PE, Green, The, Fischer CL, Ed. Kr.
Li Y, Zeng Z, K.
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    Rosen CA, Soppet DR, Carter KC
GA, Yu G, Ni J, Feng P, Young P
Hu J, Florence KA, Olsen HS, F
Moore PA, Shi Y, Lafleur DW,

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches
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OLSEN'H S.
FISCHER C L.
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BREWER L A.
MOORE P A.
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Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM,
Duan DR, Hu J, Florner K, Olsen HS, Fischer CL, Ebner R;
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
           22-AUG-1997; 97US-0056881P.
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25-SEP-1997; 97US-0056910P.
25-SEP-1997; 97US-0054761P.
26-SEP-1997; 97US-0054493.
26-MAR-1998; 98US-00149476.
17-MAR-2000; 2000US-0.190688P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RUBE/) RUBEN S M.
(ROSE/) ROSEN C A.
(SOPP/) CARTER K C.
(BEDN/) ENDRESS G A.
(YUGG/) YU G.
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New nucleic acid molecule, useful for preparing a medicament for diagnosing, preventing, treating or ameliorating a medical condition e.g., cancer.

Claim 1; SEQ ID NO 174; 256pp; English

Ø The invention describes an isolated nucleic acid comprising a sequence having 95 % identity with: a polynuclectide fragment of a sequence not given in the specification, or its allelic variant; a polynuclectide fragment of the CDNA sequence; a polynuclectide sequence encoding a polypeptide, or its fragment, domain, epitope or species homologue; or applynuclectide that hybridies under stringent conditions to any one of the sequences of (a)-(c). The nucleic acid is useful for preparing a

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for diagnosing, preventing, treating or ameliorating a medical
e.g., cancer. The sequence encodes a novel human secreted
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99.9%; Score 3169.4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3173; Conservative 0; Mismatches
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medicament for diagnosing, condition e.g., cancer. Th protein of the invention.
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	RESULT 5 ADH73891 ID ADH73891 standard; cDNA; 3173 BP.	XX AC ADH73891; xy	DT 25-MAR-2004 (first entry) XX	DE Human secreted protein cDNA #164.	e D	gene. Homo saniens	US200		10-JUN-2002; 2	07-MAR-1997; 07-MAR-1997; 07-MAR-1997;	07-MAR-1997; 07-MAR-1997;	07-MAR-1997; 07-MAR-1997; 07-MAR-1997;	11-APR-1997; 11-APR-1997;	11-APR-1997; 11-APR-1997; 11-APR-1997;	11-APR-1997; 11-APR-1997;	11-APR-1997; 11-APR-1997; 11-APR-1997;	PR 11-APR-1997; 97US-0043669P. PR 11-APR-1997; 97US-0043670P. PR 11-APR-1997; 97US-0043671P.	11-APR-1997; 11-APR-1997;	23-MAY-1997; 23-MAY-1997; 23-MAY-1997;	23-MAY-1997; 23-MAY-1997; 23-MAY-1997;	23-MAY-1997; 23-MAY-1997; 23-MAY-1997;	23-MAY-1997; 23-MAY-1997;	23-MAY-1997; 23-MAY-1997;	23-MAY-1997; 23-MAY-1997;	23-MAY-1997; 23-MAY-1997; 23-MAY-1997;	23-MAY-1997; 97US 23-MAY-1997; 97US	
Oy 2041 TCTCCAGAAGGAACTTGGGAGATGATGGTGCAGATGATGAAACTGGGTTCATCCCAGTTC 2100	2101 CAAAGACTCAGAGAACTAGAGTTTAAGCTGAGGCAGAGTGCCGCCACCTGGCATGCCCC 2160 	2161 ACAAACAGATCACCAGCTTACACAGGCATTAACTCTCCAATGAGGAAGAACAT 2220	2161 ACAAACAGATCACCAGCTTACACAGGCATTAACTCTCCTCAATGAGGAAGAATCAT 2220	2221 TCACAACTGAGCAAGACATTCATAATGATCATTTAAGGAAGTGTTTCCTTATGTTAGC 2280	tcacaactgagcaagacattcatatgatcatttaaggaagtgtttcccttatgtgtgc	2281 AAGTATAATCGGGTAACTCCTAAATCCCAATGATAGTCTAGGGTGGACAGCAATGGGC 2340 2281 AAGTATAATCGGGTTAACTCCTAAATGAATAGTCCTAAGGGTGGACAATGGC 2340	TGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCTTCTAGCAC		CAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTAGAAGATGTGCATAAT	2401 CAACIACCAITAGCACTATGITAGGAGGIGCAAGGCCCCAAAGTAGAAGATGGGCATAAT 2460 2461 GTCTGCTCTTGAGTAAGTTCAGGACAATATCCAGCACAGACACAGATAACAGTTAACAGAGAACAAAA 550	GICTGCTCTTGTGTAGCTCAGGAGACAATTCCAGCACAGACACTACAGTTAACGCTGAAC	TGCAGCTGCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGGGCAGGGCTGA	TGCAGCTGCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGGGGG	2581 AGCTGGGCCTTGAAGATGGATGGATTGAATTTGGATAGAGAAAAAAAA	2641 AAGTGAGGAGCATGAAAAATGAGCAGGGGCTGGATCAGTGGGGTTTTTTTT	2641 AAGTGAGAGAAGCATGAAAAATGAGCAGGGCCTGGATCAGGGGTGTATTCAGAGCAC 2700	2701 CTCTCCAGATGCACCATGCTCACAGTCCCTTGCCTATGTGTGGGAGAGTGTCCCAG 2760 	CCAGATGTGTGTGCCCCACCCCATGTCCATTTACATGTCCTTCAATGCCCCAC		2821 TACCTCTTCTGTAAAGCTTTCCCTGGTATCAGAATTCAAATTAATCAGGGATCTTTTCA 2880 2821 TACCTCTTCTGTAAAGCTTTCCCTGGTAATTACAAAATTAATCAGGGATCTTTTCA 2880	CACTGCTGTTTTTTCTCTTTTGGTCCTTCTATCACTAAAACTCATCTCATTCAGCCTTAC	2881 CACHGCTGTTTTTTCCTCTTCTTTCTTCTATCACTCATCTCAT	2941 AGCATAACTAATTATTTGTTTTCCTCACTACATTGTACATGGGGAATTACAGATAAACG 3000	GAAGCCKGCTGGGGTGGTGGCTCACGCTGTAATCCCAACACTTTGGGAGGCCCAAGGCG 3	3001 GAAGCCKGCTGGGGTGGTGGCTCACGCCTGTAATCCCAACATTGGGAGGCCAAGGCAG 3060	GCGGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCATNT	3061 GCGGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCATNT 3120 3121 NTACTAAAAATACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCAG 3173

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be used in the prevention, diagnosis and treatment of diseases associated with inappropriate SP expression e.g. cancer, haematopoietic disorders, canderin disorders, diseases of the immune system, inflammatory candorrine disorders, diseases of the immune system, inflammatory disorders and many others. Full details of disorders that may be consequented, disagnosed and/or treated by the above methods are given in the specification. The nucleic acid molecules may be used to proteins The nucleic acid and it's complementary sequences may also be used by presence of similar nucleic acids in samples, and therefore which cas antiques in the production of antibodies adains also be used to a antiques in need of restorative therapy. The SPS may also be used to assays to identify modulators of SP expression and activity. The anti-SP entibodies and antibodies may also be used to down regulate expression and activity. The anti-SP antibodies may also be used to down requlate expression and activity. The anti-SP antibodies may also be used as disgnostic agents for detecting the presence of the proteins in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAACCACGCCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCTTATGTAA 240
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Matches 3173; Conservative
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Duan R, Hu J, Florence KA, Olsen HS, Fischer Cl
Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y,
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                                                            Length 3299;
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                              Sequence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other;
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screening of therapeutically useful reagents
                                                          Score 3161.8;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New PRO polypeptide, useful for diagnosing and treating a B cell related disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer; immune-mediated inflammatory disease; human; gene; 88.
    CACTGCTGTTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCATTCAGTTCAGCCTTAC
                                AGCATAACTAATTATTTGTTTTCCTCACTACATTGTACATGTGGGGAATTACAGATAAACG
                                                                                                                 GAAGCCKGCTGGGGGGGGGGCTCACGCCTGTAATCCCAACACTTGGGAGGCCAAGGGAG
                                                                                                GAAGCCKGCTGGGGTGGTGGCTCACGCCTGTAATCCCAACACTTTGGGAGGCCAAGGCAG
                                                                                                                                                          GCGGATCACCTGAGGTCAGGARTTCGAGATTARTCTGGCCAACATGGTGAAACCCCATNT
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                                                                                                                                                                                                                                           NTACTAAAAATACGAAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCCAG 3173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood WI;
                                                                                                                                                                                                                        NTACTAAAAATACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 108; 695pp; English.
                                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO24934 cDNA, SEQ ID 108.
                                                                                                                                                                                                                                                                                                                                   ADL82906 standard; cDNA; 3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003; 2003WO-US029097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-2002; 2002US-0411392P.
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-329389/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004024097-A2
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Wu TD;
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ADL82906
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The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
antiniflammatory, antidarthritic, antishematic, immunosuppressive,
costeopathic, antidabetic, dermatological, antipsoriatic, antiallergic,
antiasthmatic, hepatotropic, and respiratory activity. A polymucleotide
cof the invention may have a use in gene therapy. The PRO polypeptide, its
agonist, antagonist, or antibody that specifically binds to the
cof the invention may have a use in gene therapy. The PRO polypeptide, its
agonist, antagonist, or antibody that specifically binds to the
cof upperide is useful for treating an immune related disorder such as
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
costeoarthritis, a spondyloarthropathy, systemic sclerosis, an
idiopathic inflammatory myopathy, 3/30gren's syndrome, systemic
cot sease, a demyelinating dolyneuropathy, Guillain-Barra syndrome,
cot chronic inflammatory demyelinating polyneuropathy, a hepatobilary
cot system, idiopathic demyelinating polyneuropathy, Guillain-Barra syndrome,
cot chronic inflammatory demyelinating polyneuropathy, a hepatobilary
cot inflammatory bowel disease, gluten-sensitive hepatitis, primmary
cot inflammatory bowel disease, gluten-sensitive hepatitis, primmary
cot inflammatory bowel disease, gluten-sensitive hepatitis, food
disease, arthem multiforme, contact dermatitis, psoriasis, an allergic
cot sease, asthma, allergic rhintis, antiopid disease of the lung,
cot sease, asthma, allergic rhintis, antimunologic disease of the lung,
cot sease, asthma, allergic rhintis, antimunologic disease of the lung,
contact dermatitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis, antimitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                  ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 3299 BP; 956 A; 802 C; 750 G; 791 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams PM,
                                                                                                                                                                                                                                                                                                               PRO polypeptide encoding cDNA SEQ ID NO:1120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1120; 2940pp; English.
                                                                          ВР
                                                                          ADP23942 standard; cDNA; 3299
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                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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                                                Gaps
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          Indels
Pred. No. · 0;
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98.66
           Matches 3160; Conservative
  Best Local Similarity
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Oy 2167 AGATCACCAGCTACACAGGCATTAACTCTCCTCAATGAGGAAGAATCATTCACAA 2226 Db 2161 AGATCACCAGCTTACACAGCATTAACTCTCCTCAATGAGGAAGAATCATTCACAA 2220	Oy 2227 CTGAGCAAGACATTCATATGATCATTTAAGGAAGTGTTTCCCTTATGTGTTAGCAAGTAT 2286	2287 P		2401 CCATTAGCACTATGAGAGCTGCAAGGCCCCAAAGTAGAAGATGTGATAATGTCTGC 246 2467 TCTTGTGTGAGAGAAGAAGAATTCCAGGAACAAAGACAAAGATTAACGCTGAACTGCAGC 252	2461 TCTTGTGTAGGCTCAGGAGACAATTCCAGCACAGACACTACAGTTAACGCTGAACTGCAGC 252	2521 IGCAAGTAATAGCATGAACAGTCAGAAAATACCTTATGAGGGGCAGGGGCTGAAGCTGG 258	2581 GCCTTGAAGGATGGATGAAATTTGGATAGAGAATGAGGAAGAA	2641 GAGAAGCATGAAAAATGAGCAGGCCTGGATAGTGGGGGGTGTATTCAAACAACAACACACAC	2701 AGAIGCACCAIGCAICACACACCATAGCCATGCCAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2767 GTGTGCCCCACCCATGTCCATTTACATGTCCTTCATGCCACCCAC	2827 TTCTGTAAAGGTTTCCCTGGTATCAGGAATTGATCAGGGGATCTTTTCACATGC 2	2887 IGTTTTTCCTCTTTGGTCCTTCTACACTCATCTCTCTTCAGCCTTACAGCTCT 2881 IGTTTTTCCTCTTTGGTCCTTCTATCATAAACTCATCTCATTCAGCCTTACAGCTA 2881 IGTTTTTCCTCTTTGGTCCTTCTATCAAAACTCATCTCAT	2947 ACTAATTATTTGTTTTCCTCACTACATTGTACATGTGGGGAATTACAGTGGGGGAACCC SVG 2941 ACTAATTATTTGCTCTCACTACATTGTACATGTGGGAATTACAGAAAAAGGGAAGCC 300	3001 GCTGGGGTGGCTCTCACCCCCAACCTTTGGGAGGCCAAGGCGGGT 306	<pre>Qy 3067 CACCTGAGGTCAGGARTTARTCTGGCCAACATGAAACCCCCAINTATACLA 3128 </pre>	Oy 3127 AAAATACGAAATTAGCCAGGTGTGGTGCACACATCTGTAGTCCCAG 3173 	RESULT 8 AAI72383 ID AAI72383 standard; cDNA; 3300 BP.
1021 TTGTGATCTAGGCTGCTGAGATTCTCCCTCTGGAAACTGAGTTACAACCACAATA 1080 Qy 1087 CTGGCAGGTTCCCTGGATCTTCTCTGCCCAACTCTTACTGGAAATTGCAAACT 1146 Db	CTGGCAGGTTCCCTGGATCCAGATCTTCTGCCCAACTCTTACTGGGAGATTGCAAACT 1140 GCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGCTGGGGCATAGCTTGTGCTAA 1206	1266 1260	1326 1320	1327 ITTIAUGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTCGGAAGCTGCATATGACT 1386	1387 AGAGGCCTCTTGTGACTGGAGGTAACAACCCTGCCCAGTAACTGTGGGAGAAGGGGATCA	1447 ATATTTTGCACACCTGTAATAGGCCATGGCCAAGCCAGCC	1507 GTATGTGTGAAGATCCCTGGTGCGTGGCCTTCACCACGCATCTTGAGCAAATTAGGAAAA 1566 	1567 IGTACCCTICGCTIGAGGCAGATGCAGCCCTICCCCCGAGTGCATGGCTTGGAGAGCAGA 1626	1627 ATGIGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGCAGGGCATAA 1686 	IGTGG 1746	CICTCAGCCATGTAGACACACTCTCCAAATGGAGATGTTGGAAAATGTTCTTTCT	TCTAGAGACTGCTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAGAGATTTTC 1866	GCCAT 1926 GCCAT 1920	1927 GCCCAGTATTCCCACTCTCCAAAAGGAACTGACCAGCTTATATTTCTCACACTTCTGGGG 1986 1921 GCCCAGTATTCCCACTCTCCAAAAGGAACTGACCAGCTTATATTTCTCACACTTCTGGGG 1980	AACTGGGTATAATCCAACCATCAAAATAGAAGACCTTGCAAGAAGCAGAGTCATTCTCCA 2046	AAAGA 2106	CAAAC 2166 CAAAC 2160

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing susceptibility to schizophrenia (SCZ) in a patient, by determining presence or absence of an allele of a linked polymorphic marker present on chromosome 1q22, were the marker is linked to a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was isolated using the method of the invention as the SCZ gene. This sequence has been previously identified as CD84, GenBank Accession No: NM 001874, CD84 is a 73 kDa antigen present on platelets, monocytes and circulating B cells. The proteins encoded by this sequence may be involved in the processes by which the brain responds to biological stimuli. Therefore they may provide targets for therapeutic intervention in the treatment of schizophrenia. The SCZ sequence may be used in a new method comprises determining the presence or absence of an platient. The method comprises determining the presence or absence of an allele of a linked polymorphic marker in the DNA of the patient. The polymorphic marker is present in chromosome 1422 and is linked to a gene (SCZ) having a variant form associated with a phenotype of schizophrenia
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                                                                                                    SCZ; gene; CD84; platelet; monocyte; circulating allele; polymorphic marker; chromosome 1q22; ss
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                                                                                                                         The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
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                                                                  useful for
for breast
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                                                                    cancer,
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                                                                  Novel isolated polypeptide associated with breast detecting presence of polypeptide in sample, as a
                                                                                                           Disclosure; SEQ ID NO 13255; 36pp; English.
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                                          ACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCTTATGTAACACCAGG
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DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor
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            Sequence 3326 BP; 959 A; 802 C; 753 G; 795 T; 0 U; 17 Other;
                             21; Indels
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The invention relates to treating a subject having a condition that benefits from modulating the balance of regulatory T cell function relative to effector T cell function, or vice versa, in a subject. The method involves administering an agent that modulates the expression or activity of a molecule selected from PTGER2 and TGFbetal, or Jagged-1, GPR-32, CDB3, SECTOONIN R2C, GPR63, histamine R-H4, GPR-88, EPG-R, PGG-1, PGG-3, PSG-9, PDB-4d, and PI-stamine R-H4, GPR-88, EPG-R, such that treatment occurs. The methods are useful for diagnosing, preventing or treating conditions characterized by a too-vigorous or weak effector T cell or regulatory T cell response to antigens associated with the condition, such as in an allergic response, an autoimmune disorder, a viral infection, a microbial infection, a parasitic infection or a tumour. The present sequence represents a DNA encoding a human leukocyte differentiation CD84 antigen, preferentially expressed in regulatory T cells.
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                                                                                                                                                                                                                                               Human leukocyte differentiation antigen CD84 encoding DNA.
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09-OCT-2002; 2002US-0417103P.
09-OCT-2002; 2002US-0419543P.
18-OCT-2002; 2002US-0419575P.
08-NOV-2002; 2002US-0424777P.
08-NOV-2002; 2002US-0424881P.
AD005707 standard; DNA; 1067
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                                                                                                      cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
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100.0%; Pred. No. 4.4e-307;
ive 0; Mismatches 0;
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                                                                          Human soft tissue sarcoma-upregulated DNA
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14-NOV-2002 Human CD84

AAD43563 AAD43563

RESULT 13

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The invention relates to nucleic acid molecule, designated CD2000 which encodes a polypeptide containing immunoglobulin (Ig) and Ig-like domains and SahM associated protein (SAP) morlifs. CD5000 DNA and protein is useful for treating disorder such as immune prolliferative disorders. (e.g., arthritis, multiple sclerosis, Grave's disease, and Hashinoto's disease), T cell disorder (e.g. acquired immune deficiency syndrome (ADBS)), inflammatory bowel disease (e.g. theumatory syndrome colitis), inflammatory disorders (e.g. theumatory alsorders (e.g. asthma and psoriasis), apoptotic disorders (e.g. theumatory disorders, septic shock, chronic obstructive pullmonary disease (e.g. systemic lupus erythematosus, and insulin-dependent diabetes mellitus), cytotoxic disorders, septic shock, chronic obstructive pullmonary disease (e.g. emphysema), bronchitis, cachexia, jaundice, hepatic circulatory disorders, hepatic sis section accuse myeloid leukaemia, haemophilia and anaemia. CD2000 DNA is useful in screening assays (e.g. encoders) assays Novel isolated polypeptide containing immunoglobulin and immunoglobulin-like domains and SLAM associated protein, termed CD2000 or CD2001, useful for treating immune, inflammatory, or hepatic circulatory disorders. emphysema; cachexia; hepatic circulatory disorder; hepatitis; cirrhosis; acute myeloid leukaemia; haemophilia; anaemia; gene therapy; cytostatic; immunosuppressive; neuroprotective; antinflammatory; Crohn's disease; osteopathic; antibacterial; immunomodulator; inflammatory bowel disease; jaundice; dermatological; ulcerative colitis; AIDS; CD84; gene; ds. 74 65 (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The present sequence is human CD84 DNA used in the invention CGGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGCACCACCTATGGATC CCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGCACCACCTATGGATC Gaps ; 0 Length 1040; Sequence 1040 BP; 308 A; 256 C; 231 G; 245 T; 0 U; 0 Other; Indels 9 Score 1033.4; DB 6, Pred. No. 6.6e-307;); Mismatches 1; "Human CD84 protein" Location/Qualifiers Disclosure; Page 76; 138pp; English 2000US-00706167. 02-NOV-2001; 2001EP-00309339. 32.6%; 99.9%; (MILL-) MILLENNIUM PHARM INC /*tag= a /product= /*tag= 2002-620680/67. WPI; 2002-620680, P-PSDB; AAE26238 03-NOV-2000; EP1223218-A1 17-JUL-2002. Fraser CC; Query Match Ношо Key

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This sequence represents a nucleic acid molecule designated Gene 164 from the human cDNA clone HSAWF26 (deposited as clone ATCC 97903 and ATCC 900499) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV5511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA, Fischer CL, Soppet DR, Carter KC;
P, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
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Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAVS9511 for described uses)
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New isolated human secreted protein for diagnosing, preventing, treating or ameliorating medical conditions and used as a food additive or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     preservative.
Human; ss; gene; secreted protein; autoimmune disease; chemotaxis; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; liver neoplasm cardiovascular disorder; cardiac arrest; skin aging; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorders; Alzheimer's disease; infection; nervous system disorders; necepral infection; wound healing; tissue regeneration; epithelial cell proliferation; organ transplantation; food additive; preservative; nutritional.
               Human cDNA #2 for novel secreted protein gene 164
                                                                                                                                                                                                                                                                                                9703-0043671P

9703-0043672P

9703-0047492P

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Brewer LA; Greene JM; Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC; Bednarik DR, Endress GA, Yu G, Ni J. Feng P, Young PE, Gr Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H; 9705-0047618P 9705-0047632P 9705-004964P 9705-0049910P 9705-0049910P 9705-0059126P 9705-0056631P 9705-0056631P 9705-0056632P 9705-0056632P 9705-0056632P 9705-005663P 9705-005684P 9705-005681P 97US-0058785P 97US-0061060P 98WO-US004493 (HUMA-) HUMAN GENOME SCI INC WPI; 2002-634796/68. 18-AUG-1997; 22-AUG-1997; 2-AUG-1997 22-AUG-1997; 22-AUG-1997 22-AUG-1997 22-AUG-1997 22-AUG-1997 06-MAR-1998 22-AUG-1997 22-AUG-1997 22-AUG-1997 22-AUG-1997 22-AUG-1997 22-AUG-1997

Example 1; SEQ ID NO 303; 129pp; English.

The invention relates to an isolated protein that is one of 186 human secreted proteins, given in the specification, encoded by one of 309 cDNA sequences also given in the specification. The protein is used in a pharmaceutical composition used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are disgnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative

ugo cardiac arrest, cemebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, angiogenesis, nervous system disorders e.g. Alzheimer's disease, e.g. corneal infection. The polypetides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase cordercase storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a cDNA derived from a gene encoding one of the novel human secreted proteins of the invention. Note: This sequence did not form part of the printed specification, but was obtained in electronic format directly from USPTO at e.g. neoplasms of the breast or liver, cardiovascular disorders seqdata.uspto.gov/sequence.html?DocID=6420526B1 %

Sequence 828 BP; 247 A; 198 C; 172 G; 204 T; 0 U; 7 Other;

Gaps .; : Length 828; 1; Indels Score 813; DB 6; L Pred. No. 4.7e-239; 5; Mismatches Query Match
Best Local Similarity 99.2%;
Matches 821; Conservative

2146 ACCCTGGCATGCCCCCACAACAGATCACCAGCCAGCTTACACAGGCATTAACTCTCCTCA

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CCCTTATGTGTTAGCAAGTATAATCGGCTAACTCCTAAATCCCCAATGAATAGTCCTAGGC

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AGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTA 2445 GAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGACAATTCCAGCACAGACATA 2505 300 360 241 AGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTA GAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGACAATTCCAGCACAGACACTA

2685 AGGGGCAGGCTGAAGCTGGGCCTTGAAGGATGGATGAATTTGGATAGAATGAGGA 2626 AGACAGAGGGCCTCCAAGTGAGAGAAGCATGAAAAATGAGCAGGGGCCTGGATCAGTGGG 2566 AGGGGGCAGGGCTGAAGCTTGGAAGGATGAATTTGGATAGAGAATGAGGA 421

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ALIGNMENTS

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 EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
                                                                Query Match
Best Local Similarity 100.0%;
Matches 3173; Conservative 0
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Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF I

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 60/291,949,016

FRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

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Pred. No. 0;
4; Mismatches
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Best Local Similarity 99.8
Matches 3160; Conservative
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ORGANISM: Human
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US-09-949-016-557
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| Sequence 1456, Application US/09949016
| Patent No. 6912339
| GENERAL INFORMATION:
| APPLICANT: VEXTER. VEXTER. VEXTER. VEXTER. VEXTER. VEXTER. TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| FILE REFRENCE: CLOAD1307
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 1456
| LENGTH: 3296
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Fred. No. 0;
3; Mismatches
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llarity 99.8%;
Conservative
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Best Local Similarity
Matches 3154; Conserv
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US-09-949-016-1456
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	CCGAGTGCATGGCTTGGAGAGCAGAATGTGGGGC CCGAGTGCATGGCTTGGAGAGCAGAATGTGGGG CTGCGAATCTTTGTGCAGAGCATAACAGGCTTA CTGCGAATCTTTGTGCAGAGCATAACAGGCTTA CTGCGAATCTTTGTGCAGGCATAACAGGCTTA GTGTGGGTCTCTGTCAGAGTTGTGGCTCTCAGC GTTGGAAATCTTCTGCAGAGTTGTGGCTCTCAGG GTTGGAAAATGTTCTTTCTGCAGGGTCTAGAGA GTTGGAAAATGTTCTTTCTGCAGGGTCTAGAGA GTTGGAAAATGTTCTTTCTGCAGGGTCTAGAGA GTTGGAAAATGTTCTTTTCTGCAGGGTCTAGAGA GTTGGAAAATGTTCTTTTCTGCAGGGTCTAGAGA GTTGGAAAATGTTCTTTTCTGCAGGGTCTAGAGA	1815 CTGCTGGGACATTTTCTTGGAGTGCTACTTGGAGGCTTATAGGATTTTCTTTC	2115 ACTAGAGTTTAAGCTGAGGCAGAGTGCCCCCCGGCATGCCCCCAAACAGTCACC 2174 2107 ACTAGAGTTTAAGCTGAGGCAGAGTGCCCCCCCGCAAACAGATCACC 2166 2107 ACTAGAGTTTAAGCTGAGGCGCCCCCCCGGCATGCCCCCAAACAGAGCCCC 2166 2107 ACCCAGCTTACACAGGCATTAACTCTCCCTCAATGAGAAATCATTCACAACTGAGCA 2234 2167 AGCCAGCTTACACAGCAGTTAACTCTCCCTCAATGAGAAATCATCACAACTGAGCA 2226 2235 GACATTCATATGATCATTTAAGGAAGTGTTTCCCTTATGTGTTAGCAAGTAATACGGCA 2226 2297 GACATTCATATGATCATTTAAGGAAGTGTTTCCCTTATGTGTTAGCAAGTAAATCGGCT 2286 2295 AACTCCTAAATCCCAATGAATAGTTTCCCTTATGTGTTAGCAAGTAATAGGCAGA 2354 [
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ASSOCIATED OF DETECTION AND USES THEREOF GATAAACGGAAGCCKGCTGGGG 3014 CAAGGCAGGCGCATCACCTGAG 3074 CCCCATNTNTACTAAAATACG 3134 IGTCCCAGCCAGATGTGTGCCC 2774 TCAAAAGGTACCTCTTCTGTAA 2834 ICTTTTCACACTGCTGTTTTT 2894 AGCCTTACAGCATAACTAATTA 2954 CGCTGAACTGCAGCTGCAAGTA 2534 AGGGCTGAAGCTGGGCCTTGAA 2594 GGGCCTCCAAGTGAGAAGAGCA 2654 CAGAGCACCTCTCCAGATGCAC 2714 GCATAATGTCTGCTCTTGTGT 2466 g 3173 G 3165

Db 33627 GGGATCAATATTTGCACACCTGTAATY Qy 1500 ACAGTCAGTATGTGTGAAGATCCCTGG Db 33687 ACAGTCAGTATGTGTGAAGATCCTGG Qy 1560 AGGAAAATGTACCCTTCGCTTGAGCCA Db 33747 AGGAAAATGTACCCTTCGCTTGAGCCA		
Qy 3060 GGCGGATCACCTGAGGTCAGGARTTCGAGTTARTCTGGCCAACATGGTGAAACCCCAIN 3119 Db 35247 GGCGGATCACGTCAGGTTCGAGATTAGTCTGGCCAACATGGTGAAACCCCATC 35306 Qy 3120 INTACTAAAAATACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCAG 3173 Db 35307 TCTACTAAAAATAACGAAATTAGCCAGGTGTGGTGGCACACATCTGTAGTCCCAG 35360	RESULT 5 US-00-90-016-13198 Sequence 13196, Application US/09949016 Faceure 13196, Application US/09949016 Faceure No. 6812339 GENERAL INFORMATION: FAPFILGATION TOWNERRY. J. Craig et al. TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307 CURRENT APPLICATION NUMBER: 00/241,755 FRIOR PLING DATE: 2000-10-20 FRIOR PLING DATE: 2000-10-03 FRIOR PLING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SEQ ID NO 13198 LENGTH: 37492 TTYPE: DNA CREANISM: Human US-09-949-016-13198	Deerly Match Secret 2202.8; DB 4; Length 37492;

ACARTICCAGCACAGACACTACAGTTAACGCTGAA 2519 CAGTCAGAAAATACCTTATGAGGGGGCAGGGCTG 2579 GGTGCGTGGCCTTCACCACGCATCTTGAGCAAATT 1559 33926 ACTCTCCAAATGGAGTGTTGGAAAATGTTCTTTC 1799 ACTITICITGGAGIGCTACTICAGAAGCCTIATAG 1859 TCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAG 1919 CCAAAAGGAACTGACCAGCTTATATTTCTCACACT 1979 ATCAAAATAGAAGACCTTGCAAGAAGCAGAGTCA 2039 NGGIGCAGAIGAIGAACTGGGITCATCCCAGIT 2099 34346 DGAICAITTAAGGAAGIGITTCCCTTAIGIGITAG 2279 AGCTGAGGCAGAGTGCCGCCACCCTGGCATGCCC 2159 ACAGGCATTAACTCTCCTCAATGAGGAAGAATCA 2219 TAGGCCATGGCACACCAGCCAAGATGCTCTGCTC 33686 AGATGCAGCCCTTCCCCCGAGTGCATGGCTTGGA 1619 ACACTCATCCCTTTGTCTCGGAATCTTTGTGCAG 1679 CACAGATGACAGTGCTGTGTGGGTCTCTGTCAGA 1739

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2580 AAGCTGGGCCTTGAAGGATGGATGAATTTGGATAGAGAATGAGGAAGACAGAGGGCCTC
                                                                                                                                    2640 CAAGTGAGAAGCATGAAAATGAGCAGGGGCCTGGATCAGTGGGGTGTATTCAGAGCA
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APPLICANT: Rosen et al.
TILLE OF INVENTION: 186 Human Secreted proteins
FILLE RESERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
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EARLIER APPLICATION NUMBER: 60/040,336
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
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Patent No. 6420526
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US-09-149-476-303
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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,584

R FILING DATE: 1997-05-23

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R PELING DATE: 1997-05-23 R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
R PPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,580 R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R APPLICATION NUMBER: 60/043,314
R APPLICATION NUMBER: 60/043,314
R APPLICATION NUMBER: 60/043,569
R FILING DATE: 1997-04-11
R FILING DATE: 1997-04-11
R RIGHT DATE: 1997-04-11
R RIGHT DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,311
R APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 FILING DATE: 1997-04-11 APPLICATION UNDRER: 60/043,674 APLICENT DATE: 1997-04-11 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/048,974 APPLICATION NUMBER: 60/047,583 PILLING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,617 APPLICATION NUMBER: 60/047,617 FILLING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,596 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,633 APPLICATION NUMBER: 60/047,618 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,503 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,592 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/056,886 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-04-11 FILING DATE: 1997-06-06 1997-08-22 FILING DATE: 1997-04-11 FILING DATE:

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ER APPLICATION NUMBER: 60/056,637
ER FILING DATE: 1997-08-22
ER PELING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,889
ER PILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,879
ER PILING DATE: 1997-08-22
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ER FILING DATE: 1997-08-22
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ER APPLICATION NUMBER: 60/056,894
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
R FILING DATE: 1997-08-22
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R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,892
R APPLICATION NUMBER: 60/057,761
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-28
R FILING DATE: 1997-08-28
R FILING DATE: 1997-08-29
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R PILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,576
R PILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/047,501
R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,588

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,586
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R APPLICATION NUMBER: 60/047,590
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,594
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,589
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/056,630
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,878
R APPLICATION NUMBER: 60/056,662
R APPLICATION NUMBER: 60/056,662
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,872
R APPLICATION NUMBER: 60/056,882
R APPLICATION NUMBER: 60/056,882
R APPLICATION NUMBER: 60/056,882
R APPLICATION DATE: 1997-08-22
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
FILING DATE: 1997-05-23
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
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APPLICATION UNDHER: 60/056,664
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,876
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EARLIER FILING DATE: 1997-08-22
EARLIER PELICATION NUMBER: 60/056,875
EARLIER PELING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER PILING DATE: 1997-08-22
EARLIER PELING DATE: 1997-08-22
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EARLIER PILING DATE: 1997-06-13
EARLIER PILING DATE: 1997-06-13
EARLIER PILING DATE: 1997-06-13 LING DATE: 1997-08-22 Query Match 25.6%; Best Local Similarity 99.2%; Matches 821; Conservative 2686 541 2506 421 2626 2746 2266 셤 셤 g ò g 8 용 ઠ 셤 ò 유 셤 ò 셤 ઠે ò ò a ò g ઠે ò

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Sequence 28972, Application US/09949016
; Sequence 28972, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241;755
PRIOR APPLICATION NUMBER: 60/241;755
PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILING DATE: 2000-0-0-0
; PRIOR FILING DATE: 2000-0-0-10
; RIOR FILING DATE: 2000-0-10
; SROTUMER OF SEQ ID NOS: 207012
; SOFTWARE: PASESEQ for Windows Version 4.0
; SEQ ID NO 28972
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Pred. No. 2.8e-177;
1; Mismatches 0;
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Best Local Similarity 99.8%;
Matches 600; Conservative
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US-09-949-016-28972
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                                                                                                                                                                                                                                                             | Sequence 28971, Application US/09949016
| Sequence 28971, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION NUMBER: 60/241,755 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 601
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Pred. No. 2.8e-177;
1; Mismatches 0;
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ilarity 99.8%;
Conservative
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ses 600; Conserv
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; ORGANISM: Human
US-09-949-016-28971
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Sequence 28974, Application US/09949016
; Sequence 28974, Application US/09949016
; Patent No. 691239
; GENERAL INFORMATION:
; PAPLICATY: VERTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TILE REPERBUES: CLOOl-307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR PAPLICATION NUMBER: 60/237,768
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-30
; PRIOR PILING DATE: 2000-10-09
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFUMARE: FRASESEQ for Windows Version 4.0
; SEQ ID NO 28974
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                                                                                                                GTAGAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGACAATTCCAGCACAGACA
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TITCCCTTATGIGITAGCAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTA
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                                                          AAATTTGGATAGAGAATGAGGAAGACAGAGGGCCTCCAAGTGAGAAGAAGCATGAAAATG
                                                                         2143 GCCACCCTGGCATGCCCCACAAACAGATCACCAGCCTTACACAGGCATTAACTCTCC
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Best Local Similarity 99.8%; Pred. No. 2.8e-177;
Matches 600; Conservative 1; Mismatches 0;
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US-09-949-016-28974/c
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Sequence 28973, Application US/09949016

Patent No. 6612339

GENERAL INFORMATION:

TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOL01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 28933

LENGTH: 601

LENGTH: 601
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                                                                2244 ATGATCATTTAAGGAAGTGTTTCCCTTATGTGTTAGCAAGTATAATCGGCTAACTCCTAA
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Pred. No. 2.8e-177;
1; Mismatches 0;
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99.8%;
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Best Local Similarity 99.8'
Matches 600; Conservative
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US-09-949-016-28973/C
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; ORGANISM: Human
US-09-949-016-28973
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241 ATGAAATTTGGATAGAGAATGAGGAAGACAGAGGGCCTCCAAGTGAGAGGAGCATGAAAA 182
                                                                                          61 CATGICCATTTACATGICCTTCAATGCCCACCTCAAAAGGTACCTCTTCTGTAAAGCTT 2
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                            2661 ATGAGCAGGGCCTGGATCAGTGGGGTGTATTCAGAGCACCTCTCCCAGATGCACCATGCA
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Pred. No. 2.8e-177;
1; Mismatches 0;
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US-09-949-016-49962/c
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US-09-949-016-49962
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEQ FOR WINGOMS VERSION 4.0
SEQ ID NO 28975
LENGTH: 601
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Pred. No. 2.8e-177;
1; Mismatches 0;
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2-09-949-016-28975/c
; Sequence 28975, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 99.8%;
Matches 600; Conservative
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CRGANISM: Human
US-09-949-016-28975
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Sequence 49964, Application US/09949016
; Sequence 49964, Application US/09949016
; Sequence 49964, Application US/09949016
; General Information:
    Title OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WIMBER: 60/241,755
FILE REPERENCE: CLOO01307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASSEQ for Windows Version 4.0
; FROID NO 49964
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                                                                            2326 TGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCAT
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2266 CCCTTATGTGTTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGC
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99.8%; Pred. No. 2.8e-177
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Best Local Similarity 99.8
Matches 600; Conservative
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ORGANISM: Human
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Sequence 49963, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 2070012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 49963

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99.8%; Pred. No. 2.8e-177;
tive 1; Mismatches 0;
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Matches 600; Conservative
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; Sequence 49965, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: 60/241,755
; CURRENT PILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; WUMBER OF SEQ ID NOS: 207012
; SOUTHARE: FEALSEQ for Windows Version 4.0
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Best Local Similarity 99.8
Matches 600; Conservative
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Search completed: February 6, 2005, 00:26:49 Job time: 507 secs

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Sequence 166284, Sequence 166285, Sequence 166286,

Seguence 166284, Sequence 166285, Sequence 166286 Sequence 3, App

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Sequence:

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DB 10; Length 3173;
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002D9
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 761
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 174
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| US-10-027-632-166284
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Matches 3173; Conserv
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OTHER INFORMATION:
NAME/KEY: SITE
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303, App
36774, A
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| cgn2 6/ptodata/2/pubpna/USOF NEW PUB. seq:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-882-171-174
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US-10-198-846-13255
US-10-723-860-6219
US-10-723-860-1885
US-10-73-860-1885
US-10-73-860-1885
US-09-809-391-303
US-09-809-391-303
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US-09-918-995-36774
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Maximum Match 100%
Listing first 45 summaries
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Sequence 2695, Ap Sequence 2695, Ap Sequence 700, App Sequence 114894, Sequence 114894, Sequence 30, App Sequence 1056, Ap Sequence 1056, Ap Sequence 1056, Ap Sequence 1285, Ap Sequence 1285, Ap Sequence 1285, App Sequence 372, App Sequence 372, App Sequence 8, Applis Sequence 8, Applis

Sequence 5668, Ap Sequence 5669, Ap Sequence 5668, Ap

Sequence 3, Appli Sequence 10, Appl Sequence 1564, Ap Sequence 68, Appl

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R FILING DATE: 2001-03-16

R APPLICATION NUMBER: 09/149,476

R FILING DATE: 1998-09-08

R FILING DATE: 1998-03-06

R RELING DATE: 1998-03-06

R APPLICATION NUMBER: 60/040,162

R APPLICATION NUMBER: 60/040,162

R APPLICATION NUMBER: 60/040,162

R FILING DATE: 1997-03-07

R FILING DATE: 1997-03-07
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REPLING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,600
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R APPLICATION NUMBER: 60/047,615
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,587
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
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APPLICATION WUMBER: 60/047,598
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
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APPLICATION WUMBER: 60/047,582
ELING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/043,568
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APPLICATION NUMBER: 60/043,314
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,502
FILING DATE: 1997-05-23
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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  APPLICATION NUMBER: 09/809,391
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FILING DATE: 1997-03-07
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FILING DATE: 1997-03-07
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Sequence 174, Application US/09882171
GRNEMATION NO. US200310175858A1
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT PILING DATE: 2001-06-18
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APPLICATION NUMBER: 60/047,585
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CACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCACAGAAATTATTATGAAC 300 GGATACATGCCTTAGGTCCGAACTACAATCTGGTCATTAGCGATCTGAGGATGGAAGACG 360 AAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCTTATGTAA TCGACCCCASGCGTCCGTGCTTTTCCACAGAAGGTTAGACCCTGAAAGAGATGGCTCAGC ACCACCTATGGATCTTGCTCCTTTGCCTGCAAACCTGGCAAGCAGGAGAAAAGACT CACCAGGAGACTCAGAAACAGCACCCGTAGTTACTGTGACCCCACAGAAATTATTATGAAC AAGAACCACGGCAAGTTAAAATCATTGCTTGGACTTCTAAAACATCTGTTGCTTATGTAA Gaps ; 0 0; Indels 99.9%; Score 3169.4; 100.0%; Pred. No. 0; ive 0; Mismatches PRIOR APPLICATION NUMBER: 60/047,586
PRIOR FILING DATE: 1997-05-23
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                           Length 3173;
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                             DB 17;
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                           Score 3169.4;
Pred. No. 0;
0; Mismatches
                               100.08; Pre
                             99.98;
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                           Query Match
Best Local Similarity
Matches 3173; Conserv
US-10-164-861-174
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                  2521 TGCAGCTGCAAGTAATAGCATGAACAGTCAGAAAAATACCTTATGAGGGGGGCAGGGCTGA
                                                           <u> AGCTGGGCCTTGAAGGATGGATGAAATTTGGATAGAGAATGAGGAAGACAGAGGGCCTCC</u>
                                                                            2581 AGCTGGGCCTTGAAGGATGGATGGATAGGATAGAAATTGAGAAATGAGGAAGACAGAGGGCCTCC
                                                                                                                    AAGTGAGAGAAGCATGAAAAATGAGCAGGGCCTGGATCAGTGGGGTGTATTCAGAGCAC
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FUDLICATION NO. US20030225248A1
GENERAL INFORMATION:
APPLICATION NO. 1850401
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/10/164,861
CURRENT APPLICATION NUMBER: US/09/149,476
FRICH FILING DATE: 1998-09
FRICH FILING DATE: 1998-03-08
FRICH FILING DATE: 1998-03-06
NUMBER OF SEQ ID NOS: 757
SEQ ID NO 174
LENGTH: 3173
LENGTH: 3173
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3119)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (3121)
OTHER INFORMATION: n equals a,t,g, or c
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       Sequence 13255, Application US/10198846

Publication No. US2003009974A1

GENERAL Incordantion:
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Wangyao
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR PILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13255
LINGTH: 3687
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NAME/KEY: misc_feature
LOCATION: 1, 2, 3669, 3670, 3671, 3672, 3674, 3675, 3676, 3677,
LOCATION: 3679, 3679, 3680, 3681, 3682, 3684, 3685, 3686, 3687
OTHER INFORMATION: n = A,T,C or G
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99.6%; Score 3159.8;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3158; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 6219, Application US/10723860

| Sequence 6219, Application US/10723860
| Publication No. U320040253606A1
| GENERAL INFORMATION:
| APPLICANT: Aziz, Matasha
| APPLICANT: Zlotnik, Albert |
| TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators |
| TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators |
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COCATION: (2531)..(2547)

COTHER INFORMATION: n is

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                              GGCTTAGTAAGTCCAAACACAGATGACAGTGCTGTGTGGGTCTCTGTCAGAGTTGTGGCT
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Sequence 1885, Application US/10723860

Publication No. US20040253606A1

GENERAL INFORMATION:
APPLICANT: Alzia, Natasha

TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFREENCE: 05882.0193.NPUS01

CURRENT APPLICATION NUMBER: US/10/723,860

CURRENT APPLICATION NUMBER: 00/429,739

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR APPLICATION NUMBER: 60/429,739

PRIOR PILLING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 8393

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

TYPE: DNA
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Length 1067;
                           Indels
32.6%; Score 1034; DB 18;
100.0%; Pred. No. 8.8e-309;
ative 0; Mismatches 0;
  Query Match 32.6
Best Local Similarity 100.
Matches 1034; Conservative
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CCCTTATGTGTTAGCAAGTATAATCGGCTAACTCCTAAATCCCCAATGAATAGTCCTAGGC 2325
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/809,391
CURRENT FILING DATE: 2001-03-16
FLOOR APPLICATION ARE removed - CONSULT PALM OF £5;
NUMBER OF SEQ ID NOS: 761
SEQ ID NOS: 761
SEQ ID NO 303
LENGTH: 828
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Pred. No. 2.3e-240;
5; Mismatches 1;
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US-09-809-391-303
IS-09-809-391-303
Separation US/09809391
Publication No. US20030049618A1
GENERAL INFORMATION:
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, OTHER INFORMATION: n equals a,t,g,
US-09-809-391-303
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Best Local Similarity 99.2
Matches 821; Conservative
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i Sequence 29, Application US/10436523

j Publicatation No. US2030180888A1

j Publicatation No. US2030180888A1

j GENERAL INFORMATION:

i APPLICANT: Fraser, Christopher C.

i TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

i TITLE OF INVENTION: CD2000 AND CD2001 MOLECULES, AND USES THEREOF

i FILE REFERENCE? 1863-244-999

i CURRENT APPLICATION NUMBER: US/10/007,303

PRIOR APPLICATION NUMBER: US/10/007,303

PRIOR PILING DATE: 2000-11-03

i PRIOR FILING DATE: 2000-11-03

i NUMBER OF SEQ ID NOS: 100

i SOFTWARE: PatentIn version 3.1

i LENGTH: 1040

i TYPE: DNA

i ORGANISM: Homo sapiens

US-10-436-523-29
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Pred. No. 1.3e-308;
0; Mismatches 1; Indels 0;
                                                                         1054 TAGGCTGCTGGGCT 1067
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Best Local Similarity 99.9%;
Matches 1034; Conservative
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R APPLICATION NUMBER: 60/047,596
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,612
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,632
R FILING DATE: 1997-05-23
R PELING DATE: 1997-05-23
R PELING DATE: 1997-05-23
R PELING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/043,568

R APPLICATION NUMBER: 60/043,314

R APPLICATION NUMBER: 60/043,314

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,569

R FILING DATE: 1997-04-11
               R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                              R APPLICATION NUMBER: 60/047,617
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,618
R APPLICATION NUMBER: 60/047,503
R APPLICATION NUMBER: 60/047,503
R APPLICATION NUMBER: 60/047,592
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APPLICATION NUMBER: 60/056,886
FILING DATE: 1997-08-22
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
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FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,313
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APPLICATION NUMBER: 60/043,315
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APPLICATION NUMBER: 60/047,582
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,598
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,492
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,587
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DATE: 1997-03-07
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                                                                                               241 AGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCTGCAAGGCCCCAAAGTA
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1) Sequence 303, Application US/09882171

1) Fublication No. US20030175858A1

1) GENRAL INFOMMATION:

2) APPLICANT: Ruben et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REPRENCE: PZ002022

CURRENT APPLICATION NUMBER: US/09/882,171

CURRENT PILING DATE: 2001-06-18

PRIOR PILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 09/149,476

PRIOR PILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-03-08

PRIOR FILING DATE: 1998-03-07

PRIOR PILING DATE: 1999-03-07

PRIOR PILING DATE: 1999-03-07

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,336

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,336

PRIOR PILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: 60/040,336

PRIOR PILING DATE: 1997-03-07

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NUMBER: 60/056,877 1997-08-22 NUMBER: 60/056,889 1997-08-22 1997-08-22 NUMBER: 60/056,893 1997-08-22 NUMBER: 60/056,630 1997-08-22 1997-08-22 NUMBER: 60/056,678 1997-08-22 NUMBER: 60/056,878 1997-08-22 NUMBER: 60/056,878	1997-08-22 NUMBER: 60/056 11997-08-22 11997-08-22 11997-08-22 NUMBER: 60/056	NUMBER: 60 1997-05-2 1097-05-2
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AAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGCAGGGCATAACAGGCTTAGTAAGTC 1701
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                                                                                                                                                                                                                                                                                                                                                                                         CAAACACAGATGACAGTGCTGTGTGGGTCTCTGTCAGAGTTGTGGCTCTCAGCCATGTAG 241
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                                                                                                                    601 GGCAGAGTGTCCCAGCCAGATGTGTGCCCCCCACGTCCATTTACATGTCCTTCAAT
                                                                                         2626 AGACAGAGGGCCTCCAAGTGAGAGAAGCATGAAAATGAGCAGGGGCCTGGATCAGTGGG
                                                                                                                                                                                                    541 Greratreagascaceryrecagarscacerrecarscreacacerecerrecerrater
                                                  421 AGGGGCAGGCTGAAGCTGGGCCTTGAAGGATGGATGAAATTTGGATAGAGAATGAGGA
                                                                                                                                                                   2686 GIGIATICAGAGCACCICTCCAGAIGCACCAIGCAIGCICACAGICCCTIGCCTAIGIG
                                                                                                                                                                                                                                         2746 GGCAGAGTGTCCCAGCCAGATGTGTGCCCCCACCCCATGTCCATTTACATGTCCTTCAAT
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; Sequence 36774, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
    TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FEASTES for Windows Version 3.0
; SEQ ID NO 36774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 5.6e-117;
0; Mismatches 3;
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Local Similarity 99.3%;
Les 416; Conservative
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US-09-918-995-36774
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US-09-918-995-36774
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Best Local Simil
Matches 416; (
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                                                                                                                              ATCAGGGATCTTTTCACACTGCTGTTTTTCCTCTTTGGTCCTTCTATCACTAAAACTCA 2924
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661 GCCCACCTCAAAAGGYACYTCTTCTGTAAAGCTTTCCCTKGGTATCAGGAATCAAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2206 ATGAGGAAGAATCATTCACAACTGAGCAAGACATTCATATGATCATTTAAGGAAGTGTTT
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                                                                                                                                                                                                                                                                                                                               Sequence 303, Application US/10164861

Publication No. US20030225248A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1

CURRENT APPLICATION NUMBER: US/10/164,861

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: US/09/149,476

PRIOR APPLICATION NUMBER: PCT/US98/04493

PRIOR FILING DATE: 1998-09-08

PRIOR FILING DATE: 1998-03-06

NUMBER OF SEQ ID NOS: 757

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 303

LENGTH: 928
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US-10-164-861-303
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US-10-164-861-303
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1435 AGAAGGGGATCAATATTTTGCACACCTGTAAT--AGGCCATGGCACACCAGCCAAGATGC 1492
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
OTHER INFORMATION: n equals a,t,g, or
LCCATION: (469)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LCCATION: (473)
OTHER INFORMATION: n equals a,t,g, or
LCCATION: (483)
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Publication No. US20030099974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
                                                                                                OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (435)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                 COCATION: (466)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
TOCATION: (468)
                                INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                          INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                      LOCATION: (442)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.9
Best Local Similarity 92.5
Matches 283, Conservative
                                                   NAME/KEY: misc feature LOCATION: (426)
                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (442)
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (466)
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                                                                                                                                                                                                                                                                                           Sequence 5649, Application US/09783590
| Patent No. US20020110850A1 |
| GENERAL INFORMATION: |
| APPLICANT: Dillon, Patrick J. |
| APPLICANT: Haseltine, William A. |
| APPLICANT: Li, Hacdong A. |
| APPLICANT: Rosen, Craig A. |
| APPLICANT: Rosen, Craig A. |
| APPLICANT: Rosen, Steven M. |
| APPLICANT: Rosen, Steven M. |
| TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 |
| TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 |
| TITLE OF INVENTION: NUMBER: US/09/783,590 |
| FILE REFERENCE: PO-16.2C1 |
| CURRENT APPLICATION NUMBER: 08/420,856 |
| PRIOR FILING DATE: 1994-11-21 |
| NUMBER OF SEQ ID NOS: 12485 |
| SEQ ID NO 5649 |
| LENGTH. SEQ ID NOS: 12485 |
| LENGTH. SEQ ID NOS: 12485 |
| LENGTH. SEQ ID NOS: 12485 |
| LENGTH. SEQ ID NOS: 12485 |
| LENGTH. SEQ ID NOS: 12485 |
                                              1882 TCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGCCCAGTATTCCCA 1940
242 ACACACTCTCCAAATGGAGTGTTGGAAATGTTCTTTCTGCAGGGTCTAGAGACTGCTGG 301
                                                                                           302 GACACTITICITIGGAGTGCTACTICAGAAGCCTTATAGGATTTTTCTTCCTGGCCAAGATT 361
                                                                                                                                                                       362 TCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGCCCAGTATTCCCA 420
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (370)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (406)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,'or NAME/KEY: misc feature
LOCATION: (355)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (167)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                           RESULT 12
US-09-783-590-5649
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7640 CAGGIGACATIGICTITIGGCCAAAGIGGIAICCITIATICCCAGCAGACTICIGGICCTIT 7581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 141.2; DB 15; Length 16815;
Pred. No. 2.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 184, Application US/10052482
; Dublication No. US20040072264A1
; GENERAL INFORMATION:
    APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified base

: LOCATION: (6779) .. [6878)

: OTHER INFORMATION: a, t, c, g, unknown or other

US-10-017-161-1579
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (16483)..(16615)
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                                                                                                                                                                                                                                                                                          CDS
(16030)..(16267)
                                                                                                                                                                                                                                            CDS
(9933)..(9982)
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(1687)..(1956)
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(4564)..(4707)
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(1497)..(1568)
CDS
(201)..(388)
                                             CDS (870) .. (941)
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Best Local Similarity
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US-10-052-482-184
                                             NAME/KEY:
LOCATION:
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FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 GIGAAIGGGAITCIGGGAGAGICAGICACIIIICCCIGITAAIAICCAAGAACCACGGCAA
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                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 640, 642, 643, 644, 659, 668, 675, 687, 697, 725, 726, 727,
LOCATION: 728, 735, 757, 779, 781, 790, 804, 816
OTHER INFORMATION: n = A,T,C or G
           APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT PAPPLICATION NUMBER: US/10/198,846
CURRENT PILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6370
LENGTH: 820
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6.7%; Score 212.4; DB 14; Length 820;
Best Local Similarity 96.7%; Pred. No. 2.9e-54;
Matches 238; Conservative 0; Mismatches 6; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang, Youzhen
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: source
LOCATION: (1)..(16815)
FEATURE:
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25199 GTAATCCCAGCACTTTGGGAGGCCGAGGCAGGTGATCACCTGAGGTCGGGAGTTTGAGA 25258
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                                                                                                                                                                                                                                                                                                                                                                                                                           3090 TTARTCTGGCCAACATGGTGAAACCCCATNTNTACTAAAAATACGAAATTAGCCAGGTGT 3149
                                                                                                                                                                     Query Match

4.4%; Score 140; DB 17; Length 96592;
Best Local Similarity 78.9%; Pred. No. 1.7e-30;
Matches 161; Conservative 3; Mismatches 40; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 6, 2005, 00:53:42 Job time : 1609 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25319 GGTGGCAGACACCTGTAATCCCAG 25342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3150 GGTGGCACACATCTGTAGTCCCAG 3173
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 184
; LENGTH: 96592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-482-184
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Best Local Similarity 100.
Matches 987; Conservative
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AY408982 Pan trog1
BQ712229 AGENCOURT
BQ712137 AGENCOURT
AV716814 AV716814
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EST375213
602291349
1001 Full
BP300686
BP303350
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 tcgaccccasgcgtccgtgc.....gcacacatctgtagtcccag 3173
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               sw model
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BP297015
BU429718
BP299453
BP298646
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Maximum DB seq length: 200000000
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9b htc: *
9b est3: *
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0; Gaps

31.1%; Score 987; DB 9; Length 987; 100.0%; Pred. No. 3.3e-210; tive 0; Mismatches 0; Indels

1. .987
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/db_xref="taxon:9606"

<1. ... >987 /gene="CD84" /locus_tag="HCM3405"

110

51 ATGGCTCAGCACCATATGGATCTTTGCTCTTTGCCTGCAAACCTGGCCGGAAGCAGCT

ò

GI:39764950

2.1

AY408982

987 bp DNA linear GSS 15-DEC-2003
Pan troglodytes CD84 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

AY408982

RESULT 2
AY408982
LOCUS
DEFINITION

ACCESSION

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troglodytes (chimpanzee)
troglodytes
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malla; Butheria; Primates; Catarrhini; Hominidae; Pan.
(bases 1 to 987)
trk, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
d, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
riera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
ariora, S., Wang, G. Shouldion from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                    (bases 1 to 987)

Kk,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Jh.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

tiera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

ms,M.D. and Cargill,M.

ms,M.D. and Cargill,M.

set Submission

nitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

kville, MD 20850, USA

s sequence was made by sequencing genomic exons and ordering

n based on alignment.

Location/Qualifiers
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/organism="Pan troglodytes"
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E 1 (bases I to 916)

IN INH-MGC http://mgc.nci.nh.gov/.

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov Watson

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2473 row: e column: 10

High quality sequence stop: 588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="INAGE:6281073"
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ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                         AGENCOURT 8354629 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281073 5', mRNA Sequence.
                                                                                                                                                                                                                                                                                                                        GAAGTGCAGTTTGCTGATAAGATGGGGAAAGCCAGCACACAGGACAGTAAACCTCCTGGG 1010
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GAAAAGAATGTGACATACAATTGGAGTCCCCTGGGAGAAGAGGGGTAATGTCCTTCAAATC
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                                                                                   ACTCACCACACAGGGTTGCTGAGCGTGCTTGCTATGTTCTTCTGCTTGTTCTCATTCTG
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                    BQ712229.1 GI:21851128
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GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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                                                                                                              Score 836.6; DB 5; Length 916;
Pred. No. 1.7e-176;
0; Mismatches 14; Indels 5.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E. (Bases I to 634)

Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z. and Han, Z.

Lu, G., Cheng, Z. and Han, Z.

Lu, G., Cheng, Z. and Han, Z.

Lu, G., Cheng, Z. and Han, Z.

Lu, G., Cheng, Z. and Han, Z.

Lu, G., Cheng, Z. and Han, Z.

Lu, G., Cheng, Z.

Homo sapiens cDNA DCB clones

Contact: Zeguang Han

Contact: Zeguang Han

Contact: Zeguang Han

Contact: Zeguang Han

Sig Guo, Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Z01203, P. R. China

Fax: 86-21-50801992
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                    TTAGCAAGTATAATCGGCTAACTCCTAAATCCCAATGAATAGTCCTAGGCTGGACAGCAA 372
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/note="Vector: pTriplEx2; Site_l: sfilA; Site_2: sfilB"
                                                                               373 TGGGCTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGAATCCATAGACTCATCT
                                                                                                                                                            ATAATGTCTGCTCTTGTGTGTGTCAGGAGACAATTCCAGCACAGACACTACAGTTAACGC
                                                                                                                                                                                                                                                                                             ATAATGTCTGCTCTTGTGTGTAGCTCANGAGACAATTCCAGCACAGACACTACAGTTAACGC
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                                                           TGGGCTGCAATTAGGCAGATAAAGACATCAGTCCCAGTAAATGGAATCCATAGACTCATCT
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This clone is available at CHGC in Shanghai
Location/Qualifiers
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llarity 98.3%; Pred. No. 3.1e-128;
Conservative 3; Mismatches 8;
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/organism="Homo sapie:
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="BM25.8"
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                                                                                                                                                                                                                              Homo sapiens Eukaryota, Matazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 890)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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High quality sequence stop: 490.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
CAAAAGCCTAATAGAATTT 915
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BQ712137.1 GI:21851036
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1000)
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NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLCM251 row: k column: 06

High quality sequence start: 54

High quality sequence stop: 539.

Location/Qualifiers

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                   CTTGCCTATGTGGCAGAGTGTCCCAGCCAGATGTGTGCCCCCCACCCCATGTCCATTTA
                                                            2613 TAGAGAATGAGGAAGACAGAGGCCTCCAAGTGAGAAGAGCATGAAAAATGAGCAGGGGC
1 ATCACAGACGGTACAGGTAACGCTGAACTGCAGCTGCAAGTAATAGCATGAACAGTCAGA
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Homo sapiens
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Pred. No. 5.2e-128;
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Best Local Similarity 95.2%;
Matches 692; Conservative (
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2429
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602291349F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4385965 5',
481 ANTTAAAGAAGTGTTTCCCCTATGTGTTAGCAAGTATAATCGGCTAACTCCTAAAATCCA 540
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tious="limate: https://www.cell line"
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10068 row: b column: 14

High quality sequence stop: 638.

Location/Qualifiers
                                                                                                                                             2310 ATGAATAGTCCTAGGCTGGACAGCAATGGGCTGCAATTAGGCAGATAAAGACATCAGTCC
                                                                           541 AAGAATAGTCCTAAGCTGGACAGGCATGGGCTTGCATTATGCAGATTAAGACATCTAATC
                                                                                                                       2370 CAGTAAATGAATCCATAGACTCATCTAGCACCAACTACCATTAGCACTATGTTAGGAGCT
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ilarity 87.4%;
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Matches
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AUTHORS
TITLE
JOURNAL
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mRNA sequence.
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                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
Hegde, P., Qi,R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                              Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fat: 301 838 3528

Fax: 301 838 0208

Bmail: johnq@tigr.org
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                             666 bp mRNA linear
EST375213 MAGE resequences, MAGH Homo sapiens cDNA,
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Pred. No. 1e-126;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone lib="MAGE resequences, h
/note="Vector: pBluescriptsKm"
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Best Local Similarity 95.2%;
Matches 633; Conservative
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Homo sapiens
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//note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse CDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
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/db_xref="taxon.9606"
/tismue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
Collection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 19.1%; Score 606; DB 7; Length 608; Local Similarity 100.0%; Pred. No. 7.8e-125; nes 606; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                            Plate: 11032 row: 11 column: E Seq primer: ACTGGGCGTCGTTACAAGGTCGTGGCTGGTTACAAGGTCGTGGCTGGAAAC High quality sequence stop: 607
way Smith 858, BOSTON, MA 02115,
                                                                                                                                                                 FORWARD: ATGGCTCAGCACCACCTA
BACKWARD: TAGATCACAATTTCATAGCTTGAAGT
INSERT LENGTh: 608 Std Error: 55.00
Plate: 11032 row: 11 column: E
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/organism="Homo sapiens"
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Hobses I to 608)

Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerara,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
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591 TTCCAGACT 541 TTCCAGACT	Oy 651 AACAAT 656 Db 601 AACAAT 606	RESULT 10 BP300686 LOCUS BP300686 BP300686 BP300686 Sygano CDNA library, macrophage Homo sapiens CDNA clone	ACCESSION BP300686 VERGION BP300686.1 GI:52229646 KEYWORDS EST. COUNTER HOMO SAPIES (human)	OKGANISM HOMO Sapiena Dikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 598)	AUTHORS SUZUKLI,, TAMBBILLA,K., SHITOCA,M., SAKAKLDARA,Y., CHIDA,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S. TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	JOURNAL Genome Res. 14 (9), 1711-1718 (2004) COMMENT Contact: Yutaka Suzuki Department of Virology	Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ins.u-tokyo.ac.jp. FEATURES Location/Qualifiers		/clone_lib="Sugano cDNA library, macrophage"	Query Match 18.4%; Score 585; DB 5; Length 598; Best Local Similarity 99.8%; Pred. No. 4e-120; Matches 596; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	OY 1079 CACCAATACTGGCAGGTTCCCTGGATCTTCTCTGCCCAACTCTTACTGGGAGAT 1138	OY 1139 TGCAAACTGCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGCTGGCGGATAGCTT 1198 Db 61 TGCAAACTGCCACATCTCAGCCTGTAAGCAAAGCAGGAAACCTTCTGCTGGGGATAGCTT 120	Qy 1199 GTGCCTAAATGGACAAATGGATGCATACCCTCCTGAAATGACTCCCTTCTGAATGAA	Qy 1259 ACAAAGCAGGTTACCTAGTATAGTTTCCCAAACTTCTTCCCATCATAGCACATGTAGAA 1318 	QY 1319 AATAATTTTTATGGCACACTGGGATAAACAAGCAAGATTGCTCACTTCTGGAAGCTGC 1378 	OY 1379 ATATGACTAGAGGCTCTTGTGACTGGAGGTAACAACCCTGCCCAGTAACTGTGGGAGAA 1438	OY 1439 GGGGATCAATATTTGCACACCTGTAATAGGCCATGGCACACCAGCCAAGATGCTCTGCT 1498

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BU429718 590 bp mRNA linear EST 09-SEP-2002 UI-HF-BN0-aen-f-02-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3064850 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/cell_type="germinal center B cells"
/cell_tine="MGCBS"
/cell_tine="MGCBS"
/clone_lib="NIH_MGC_SO"
/note="Vector: pT7T3-Pac; Site_l: Not1; Site_2: Eco RI;
constructed from size fractionaled cytoplasmIc mRNA
(3.5-4.4kb): Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Patima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
2432 AAGGCCCCAAAGTAGAAGATGTGCATAATGTCTGCTCTTGTGTAGCTCAGGAGACAATTC
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Gontact: Robert Strausberg, Ph.D.
Email: cgapber@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution informatio
found through the I.M.A.G. E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M.3 Forward.
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Best Local Similarity 99.1%; Pred. No. 8.7e-119;
Matches 582; Conservative 0; Mismatches 5;
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/clone="IMAGE:3064850"
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Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 580)

S suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima. Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

L Genome Res 14 (9), 1711-1718 (2004)

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Heal: Spanukiénisus. Hinatoku, Tokyo 108-8639, Japan

Email: ysuzukiénisus. Leokyo.ac.jp.
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                                                                          624 ACGTGTACAGCCCAGAACCCTGTCAGCAACAATTCTGACTCCATCTCTGCCCGGCAGCTC
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                                                    564 GGAGAAGAGGCTAATGTCCTTCAAATCTTCCAGACTCCTGAGGACCAAGAGCTGACTTAC
                                                                                                                                                          TGTGCAGACATCGCAATGGGCTTCCGTACTCACCACCGGGTTGCTGAGCGTGCTGGCT
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100.0%; Pred. No. 5.2e-119;
iive 0; Mismatches 0; Indels
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="MPC02331"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dassa 1 to 583)

Suzuki, Y. Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizubima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

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Institute of Medical Science, University of Tokyo
4-6-1, Shirokamedai, Minatoku, Tokyo 108-8639, Japan
Email: Location/Qualifiers
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                          Score 577.8; DB 5;
Pred. No. 1.6e-118;
0; Mismatches 2;
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/mol_type="mRNA"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Es Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,R. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
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Email: ysuzuki@ims.u-tokyo.ac.jp.
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BP299453 Sugano cDNA library, macrophage Homo sapiens cDNA clone MPC08221, mRNA sequence.
GCCAAGATTTCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCCATGCCCAG 1932
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                            GAGGGTGGGACACTTTTCTTGGAGTGCTACTTCAGAAGCCTTATAGGATTTTCTTCTTG
                                                                                                                                             GCCAAGATTTCCTTCTGTATCACTCCAAGCAGCCTCAGCAGAAGAAGCAGCAGCCATGCCCAG
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/clone="wRC08221"
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/cell_type="macrophage"
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1620 GAGCAGAATGTGGGGCTGCATATAAGCACACTCATCCCTTTGTCTGGGAATCTTTGTGCAG 1679
101 GAGCAGAATGTGGGCTGCATATAAGCACACTCATCCTTTTGTCTGGGAATCTTTGTGCAG 360
                                                                                                                                                                                                                                                                                                                   1439
                                                                                                                                                                  1499
                                                                                                                                                                                                     1560 AGGAAAATGTACCCTTCGCTTGAGGCAGATGCAGCCCTTCCCCCGGTGCATGGTTGGA 1619
241 AGGAAAATGTACCCTTCGCTTGAGGCAGATGCAGCCCTTCCCCCCAGTGCATGGTTGGA 300
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                                                                                                                                                                1440 GGGATCAATATTTTGCACACCTGTAATAGGCCATGGCACACCAGCCAAGATGCTCTGCTC 1499
                                                                                                            9
                                                                                                                              0; Gaps
                                                        Length 583;
/db_xref="taxon:9606"
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/cell_type="macrophage"
/clone_lib="Sugano_cDNA_library, macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.2%; Score 576.6; DB 5; Length Best Local Similarity 99.3%; Pred. No. 3e-118; Matches 579; Conservative 0; Mismatches 4; Indels
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